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# SUMMARIES

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# ALIGNMENTS

JOURNAL FEATURES	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AR091102/c	RESULT 1
Patent: US 594076-A 1222 30-NOV-1999; Location/Qualifiers	Methods of assaying differential expression	Chenchik, A., Jokhadze, G. and Bibliashvilli, K.	1 (bases 1 to 28)	Unclassified.	Unknown.	Unknown.		AR091102.1 GI:10017857	AR091102	Sequence 1222 from patent US 59940/6.	AR091102 28 bp DNA linear FAR 0/-SEF-2000		

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Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
Methods of assaying differential expression
Patent: US 594076-A 1221 30-NOV-1999;
Location/Qualifiers
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Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
Methods of assaying differential expression
Patent: US 6352829-A 1222 05-MAR-2002;
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Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
Methods of assaying differential expression
Patent: US 6352829-A 1221 05-MAR-2002;
Location/Qualifiers
1 (bases 1 to 20)
Ackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, Ackermann and Marcusson, Antisense modulation of novel anti-apoptotic bcl-2-related Patent: US 6001992-A 2 14-DEC-1999;
Location/Qualifiers
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Unclassified.
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Ackermann.E.J., Bennett,C.Frank., Dean,N.M. a
Antisense modulation of novel anti-apoptotic
Patent: US 6001992-A 17 14-DEC-1999;
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Ackermann,E.J., Bennett,C.Frank., Dean,N.M. a
Antisense modulation of novel anti-apoptotic
Patent: US 6001992-A 3 14-DEC-1999;
Location/Qualifiers
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Ackermann, E.J., Bennett, C.Frank., Dean, N.M. a Antisense modulation of novel anti-apoptotic patent: US 6001992-A 4 14-DEC-1999;
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Ackermann, E.J., Bennett, C.Frank., Da Antisense modulation of novel anti-patent: US 6001992-A 5 14-DEC-1999;
Location/Qualifiers
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Ackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, EACkermann and Marcusson, Eackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, Eackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, Eackermann, E.J., Bennett, Dean, N.M. and Marcusson, Eackermann, E.J., Bennett, Dean, N.M. and Marcusson, Eackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, Eackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, Eackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, E.J., Bennett, C.Frank., Dean, 
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Ackermann,E.J., Bennett,C.Frank., Dean,N.M. & Antisense modulation of novel anti-apoptotic patent: US 6001992-A 6 14-DEC-1999;
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1 (bases 1 to 20)

Ackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, E.G. Antisense modulation of novel anti-apoptotic bcl-2-related proteins Patent: US 6001992-A 9 14-DEC-1999;
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Ackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, E.G.
Antisense modulation of novel anti-apoptotic bcl-2-related proteins
Patent: US 6001992-A 8 14-DEC-1999;
Location/Qualifiers
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PAT 08-SEP-2000
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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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SOURCE
ORGANISM
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VERSION
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AR095058/c
LOCUS
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SOURCE
Search completed: March 14, 2003, 07:13:17 Job time: 1363.8 secs
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TITLE
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                                                                                                     Query Match
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Best Local Similarity
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                                              AAGAAACTTCTACGACAGCA 1
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ACKETMANN.E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.

Antisense modulation of novel anti-apoptotic bcl-2-related proteins patent: US 6001992-A 11 14-DEC-1999;

Location/Qualifiers
                                                                                                                                                                                                                                                                                         Sequence 11 from patent US
AR095058
AR095058.1 GI:10022567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 20)
Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
Antisense modulation of novel anti-apoptotic bcl-2-related proteins
Patent: US 6001992-A 10 14-DEC-1999;
                                                                                                                                                                                                                                                         Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified
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                                                                                                     Similarity
                                                                                                                                                                                                                                             Unclassified.
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7 c 3 g
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Pred. No.
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Run

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Copyright

Scoring table: Perfect score: Title:

US-09-869-894-1 780

Word size

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Minimum DB seq length: 0 Maximum DB seq length: 50 Total number of hits satisfying

7, Appli 3, Appli 3, Appli 48, Appli 254, Appli 254, Appli 60, Appli 30, Appli 30, Appli 30, Appli 31, Appli

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Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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                               US-08-859-998-1222
US-08-859-998-1222
US-08-859-998-1221
US-09-225-568-17
US-09-226-568-2
US-09-226-568-3
US-09-226-568-4
US-09-226-568-6
US-09-226-568-7
US-09-226-568-8
US-09-226-568-9
US-09-226-568-11
US-09-226-568-11
US-09-226-568-11
US-09-226-568-11
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US-09-226-568-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search time 18.863 Seconds (without alignments)
12681.353 Million cell updates/sec
            Sequence 1222, Ap
Sequence 1221, Ap
Sequence 1221, Ap
Sequence 1721, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 7, Appli
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Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 15, Appli
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Sequence 10, Appli
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Sequence
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US-08-859-998-1222/c
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                                                              ; OTHER INFORMATION: US-08-859-998-1222
                                                                                                                                                               ATTORNEY AGENT INFORMATION:
ANTORNEY AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEPHONE: 415-824-0875
INFORMATION FOR SEQ ID NO: 1222:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibilashvill1 Robert
APPLICANT: Bibilashvill1 Robert
APPLICANT: Bibilashvill1 Robert
APPLICANT: Bibilashvill1 Robert
ATTILE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FasteSQ for Windows Version
CURRUT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                          MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 21-MAY-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson, P.C. STREET: 2200 Sand Hill Road, Suite 100 CITY: Menlo Park STATE: CA COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                        TOPOLOGY:
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PCT-US94-5821A-7
US-08-598-591-71
US-08-598-706-48
US-08-117-952-54
US-08-117-952-54
US-08-117-952-54
US-08-607-384A-30
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US-08-98-27-21
US-08-98-706-31
US-08-988-706-31
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US-08-988-706-31
US-08-988-706-31
US-08-988-706-31
US-09-255-154D-31
US-08-928-941D-34
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US-08-165-761-9
US-08-165-761-9
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    Score 28;
Pred. No.
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    DB 2; L
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                          Length 28;
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Query Match Length

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US-09-225-928-1222/c

Sequence 1222, Application US/09225928

; Patent No. 6352829

; GENERAL INFORMATION:

APPLICANT: Chenchik, Alex
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US-08-859-998-122I
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SEQUENCE DESCRIPTION: SEQ ID NO: 1222:
US-09-225-928-1222
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    Sequence 1221, Application US/08859998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibliashvilli, Robert
                                                                                                                                                                                                                                                                    Matches 28;
                                                                                                                                                                                                                                                                                Query Match 3.6%;
Best Local Similarity I00.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEPAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1222:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        COMPUTER: IBM Compatible
opERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/859,998 FILING DATE: 21-MAY-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jokhadze, George
Bibilashvilli, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Field, Bret E. REGISTRATION NUMBER: 37,620
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 7.2e-05;
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US-09-225-928-I22I
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                                                                                                                                                                                                                                                                                                                                                        Sequence 1221, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.3%;
Best Local Similarity 100.0%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 0909
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-922-5070
TELEPHAX: 415-854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1221:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHOD OF AS
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2200 San
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
COUNTRY: US
ZIP: 94025
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                      NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
CAPACTESSE: Fish & Richardson,
STREET: 2200 Sand Hill Road, 5
                                                                                                                                                                                                                                                                                  Bibilashvilli, Robert TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chenchik, Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94025
                                                                                                                                                    CITY: Menlo Park
STATE: CA
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                                                                                                                                                                                                                                                                  EXPRESSION
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SEQUENCE DESCRIPTION: oligonucleotide primer (US-09-225-928-1221)
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                                                  RESULT 6
US-09-226-568-2/c
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                                                                                                                                                                                  Query Match
Best Local Similarity
"heas 22; Conserv?
                                                                                                                             В
Sequence 2, Application Patent No. 6001992 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 17
LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Micholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
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INFORMATION FOR SEQ ID NO: 1221:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                663 ACGATTGCCAACACATACTTCT 684
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                                                                                                                           Local Similarity
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REGISTRATION NUMBER: 37,620

REFERENCE/DOCKET NUMBER: 09096/002001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-322-5070
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APPLICATION NUMBER: 08/859,998
FILLING DATE: 2I-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                     DNA
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                 2.8%;
100.0%;
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                                                                                                                                                                                                                       Score 22;
; Pred. No.
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                       DB 3;
0.081;
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FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: antisense
OTHER INFORMATION: sequence
US-09-226-568-2
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US-09-226-568-3/c
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US-09-226-568-4/c
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GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Marcusson, Eric G.
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CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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Best Local S
Matches 20
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Patent No. 6001992
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Best Local (
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APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
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APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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ilarity IOO.0%;
Conservative (
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CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
SEQ ID NO 5
TYPE: DNA
TYPE:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 600
TITLE OF INVENTION: Antisense Modulation of No. 600
TITLE OF INVENTION: Antisense Modulation of No. 600
TITLE REFERENCE: ISPH-0337
CURRENT FILME DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
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US-09-226-568-6/c
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US-09-226-568-5/c
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
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CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ilarity 100.0%;
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Pred. No.
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Pred. No. 0.85;
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APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Macousson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No.
TITLE OF INVENTION: Boll-2-Related Proteins
FILE REFERENCE: ISPH-037
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
SEQ ID NO 8
SEQ ID NO 8
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Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Marcusson, Eric G.
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US-09-226-568-8/c
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US-09-226-568-7/c
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; OTHER INFORMATION: Description of Artificial Sequence: antisense; OTHER INFORMATION: sequence
US-09-226-568-6
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EILE REFERENCE: ISPH-0337

CURRENT APPLICATION NUMBER: US/09/226,568

CURRENT FILING DATE: 199-01-07

NUMBER OF SEQ ID NOTE: 39

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7
                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09226568 Patent No. 6001992
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Best Local Similarity
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LENGTH: 20
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TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-226-568-9/c
US-09-26-568-9/c
; Sequence 9, Application US/09226568
; Patent No. 6001992
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US-09-226-568-10/c
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OTHER INFORMATION: Description of Artificial Sequence: antisense; OTHER INFORMATION: sequence US-09-226-568-10
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CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 20
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LENGTH: 20
TYPE: DNA
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APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
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Best Local (
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                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic TITLE OF INVENTION: bc1-2-Related Proteins FILE REFERENCE: ISPH-0337 CURRENT APPLICATION NUMBER: US/09/226,568 CURRENT FILING DATE: 1999-01-07 NUMBER OF SEQ ID NOS: 39 NUMBER OF SEQ ID NOS: 39 NUMBER OF SEQ ID NOS: 39 NOTEN NO 10 CENT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
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                                                                                                                                          ORGANISM: Artificial Sequence
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US-09-226-568-11/c
Search completed: March 14, 2003, 08:31:49
Job time : 21.863 secs
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APPLICANT: Marcusson, Fric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION UNMERS: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEO ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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Maximum DB seq length: 50
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match Length
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2: //cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
3: //cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: //cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: //cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: //cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
7: //cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: //cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: //cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: //cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: //cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
12: //cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: //cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
14: //cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
13: //cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
14: //cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
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                            0 US-09-854-883-248
0 US-09-752-639-24
0 US-09-951-536-6
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0 US-09-951-536-6
0 US-09-963-521-6
0 US-09-899-381-34
10 US-09-899-381-34
10 US-09-804-690-17
9 US-10-092-140-4
9 US-09-734-672-60
9 US-09-734-672-60
9 US-09-734-672-60
9 US-09-982-828-60
9 US-09-982-828-60
9 US-09-980-631-81
                                                                                                                                                                                                                                                                                         US-09-834-721-6
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Sequence 6, Appli
Sequence 24, Appl
Sequence 24, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 34, Appl
Sequence 37, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 60, Appl
Sequence 81, Appl
Sequence 81, Appl
Sequence 81, Appl
Sequence 81, Appl
Sequence 82, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
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Database

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-19	US-09-747-377-359	US-10-206-654-1	US-09-930-251-9	US-09-782-650-19	US-09-782-650-18	- 1	528-2	US-09-943-851A-20	-654-2	-762	US-09-944-432-20	-097	-396-	US-09-945-015-20	US-09-945-587-20	US-09-944-457-20	US-09-944-449-20	US-09-866-028-20	US-09-841-366A-58	US-10-024-018-1	US-09-944-929-20	US-09-944-907-20	US-09-944-944-20	-944-8		
Sequence 192, App	Sequence 359, App	1, 2	Sequence 9, Appli	Sequence 19, Appl		Sequence 16, Appl	Sequence 2, Appli	Sequence 20, Appl	Sequence 20, Appl	Sequence 20, Appl	20,	Sequence 20, Appl	20,	Sequence 20, Appl	Sequence 20, Appl		Sequence 20, Appl	Sequence 20, Appl	Sequence 58, Appl			•	Sequence 20, Appl	•	`	

Title: Perfect score:

Scoring table: Sequence:

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

# ALIGNMENTS

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RESULT 2
US-09-854-883-248/c
US-09-854-883-248/c
; Sequence 248, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsert
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: DE 100 26 494.8
PRIOR FILING DATE: 2000-05-27
PRIOR FILING DATE: 2000-05-27
PRIOR PRIOR DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 6
LENGTH: 20
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-09-834-721-6/c
                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial OTHER INFORMATION: primer US-09-834-721-6
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: RIEPING, MECHTHILD
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
FILE REFERENCE: 21123/280169/MAS
CURRENT APPLICATION NUMBER: US/09/834,721
CURRENT FILING DATE: 2001-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                  Local Similarity 100.0%; P
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%; Pred. No. 1.8
0; Mismatches
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1.8e+03;
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Result No.

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us-09-869-894-1.oliszlm50.rnpb

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; OTHER INFORMATION: Antisense Oligonucleotide US-09-854-883-248
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US-09-752-639-24/c
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Best Local 9
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LENGTH: 20
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TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
FILE REFERENCE: 159H-0516
CURRENT APPLICATION NUMBER: US/09/854,883
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/629,644
PRIOR APPLICATION NUMBER: US 09/629,644
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-01-18
RIOR FILING DATE: 2000-01-18
UNMBER OF SEQ ID NOS: 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gatanaga, T.
APPLICANT: Granger, GA.
APPLICANT: Granger, GA.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                  REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
                                                                                                                                                           APPLICATION NUMBER: 09/081,385
FILING DATE: 08/964,747
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION UNMBER: 60/030,761
FILING DATE: 06-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TELEPHONE: 650 L.
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 755 PAG
CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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Madeline M. Bu
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Pred. No. 1.8e+03;
                                                                               22000-20577.21
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US-09-984-198-24
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US-09-984-198-24/c
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Matches 14;
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                                                                                                                                                                  TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,198
                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                            NAME: W. Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/30,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
FILING DATE:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS: 154
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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               Y Match 1.8%;
Local Similarity 100.0%;
                                                                                             LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                         TELEPHONE: 650 -494-0792
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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Local Similarity 100.0%;
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Conservative
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0; Mismatches
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               Score 14; DB 10;
Pred. No. 1.8e+03;
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Pred. No. 1.8e+03;
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                              Length 20;
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341 GAATTGTAACCATA 354

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APPLICANT: ZIEGLEN, DETRA
APPLICANT: EIGGLEN, LOTHAR
APPLICANT: SEGLING, LOTHAR
APPLICANT: SEAH, HERMANN
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE
TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PROPERTY.

CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: DE 199 41 478.5
PRIOR APPLICATION NUMBER: DE 199 41 478.5
PRIOR APPLICATION NUMBER: DE 199 41 478.5
PRIOR FILING DATE: 1999-09-01

NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN PROFILED TO SOFTWARE: PATENT PROFILED TO SOFTWARE: PATENTIN PROFILED TO SOFTWARE SOFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-963-521-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NEW NUCLECOTIDE SEQUENCES CODING FOR THE THRE GENE AND TITLE OF INVENTION: PROCESS FOR THE ENGYMATIC PRODUCTION OF L-THREONINE TITLE OF INVENTION: USING CORVNEFORM BACTERIA FILE REFERENCE: 21123/282414/MAS CURRENT APPLICATION NUMBER: US/09/951,536 CURRENT APPLICATION NUMBER: US/09/951,536 CURRENT FILING DATE: 2001-09-14 PRIOR APPLICATION NUMBER: 09/431,099 PRIOR APPLICATION NUMBER: 09/431,099 PRIOR FILING DATE: 1999-11-01 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09951536 Patent No. US20020107378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09963521
Patent No. US20020146781A1
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Best Local S
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APPLICANT: EGGELING, LOTT
APPLICANT: SAHM, HERMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                            Query Match
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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Local Similarity 100.0%; es 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGGELING, LOTHAR SAHM, HERMANN THIERBACH, GEORG
                                            Score 14; DB 10;
; Pred. No. 1.8e+03;
        0;
        Mismatches
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GENERAL INFORMATION:
APPLICANT: DELENSTRR, GLENDA C.
APPLICANT: LEEKOMITZ, STEVEN M.
APPLICANT: LUEBKE, KEVIN J.
APPLICANT: OVERMAN, LESLIE B.
APPLICANT: SAMPRAS, NICHOLAS M.
APPLICANT: SAMPSON, JEFFREY R.
APPLICANT: WOLBER, PAUL K.
APPLICANT: WOLBER, PAUL K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-398-399-34
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                                                                                                                                                             ; OTHER INFORMATION: synthetic probe US-09-899-381-34
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                                    δõ
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SEQ ID NO 34
LENGTH: 25
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GENERAL INFORMATION:

APPLICANT: Delenstarr, Glend C.

APPLICANT: Wolber, Pual K.

APPLICANT: Sana, Theodore R.

APPLICANT: Sana, Theodore R.

TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: 10010760-1

CURRENT APPLICATION NUMBER: US/09/899,381

CURRENT APPLICATION NUMBER: US/09/899,381
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                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/398,399
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 34, Application US/09899381 Patent No. US20020068293A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: TECHNIQUES FOR ASSESSING NONSPECIFIC BINDING OF NUCLEIC TITLE OF INVENTION: ACIDS TO SURFACES FILE REFERENCE: 10981620-1 CURRENT APPLICATION NUMBER: US/09/398,399 CUGRENT FILING DATE: 1999-09-17 NUMBER OF SEQ ID NOS: 35
                                                                                                    Query Match
Best Local :
                                                                               Matches
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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                                         531 ATCTGGCTGGATGA 544
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ATCTGGCTGGATGA 25
                                                                           Ch 1.8%; Score 14; DB 10; 1 Similarity 100.0%; Pred. No. 1.8e+03; 14; Conservative 0; Mismatches 0;
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US20020051973A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 14; DB 10; 1
100.0%; Pred. No. 1.8e+03;
ive 0; Mismatches 0;
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                                                                                                                           Length 25;
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RESULT 10
US-09-804-690-17
Sequence 17, Application US/09804690
Patent No. US20020034743A1
GENERAL INFORMATION:
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US-10-083-168-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.08;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 GAGCCAGCTCAAGA 55
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                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/804,690
FILING DATE: 12-Mar-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
NAME: SHERWOOD, Pamela J.
REGISTRATION NUMBER: 36,677
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH AND RICHARDSON, P.C.
STREET: 2200 SAND HILL ROAD
                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LI, Limin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: MENLO PARK
STATE: CA
COUNTRY: USA
                                                                                                                                                                                             APPLICATION NUMBER: 09/146,187 FILING DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Behan, Dominic P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ortuno, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10083168
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Pred. No. 1.9e+03
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US-10-092-140-4
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                                                       US-10-092-140-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IELEX: 910 277299
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 514 4845-7126
TELEPAX: 514 288-8389
TELEPAX: 514 288-8389
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Query Match
Best Local Similarity
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Best Local :
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FILING DATE: 09-Unn-1999
APPLICATION NUMBER: 60/03,374
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: 60/047,322
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: CTt, France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/092,140
FILLING DATE: 06-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Canada ZIP: H3A 2Y3
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
                                                                        TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McGill UITITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                            LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Montr, al
STATE: QC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SWABEY OGILVY RENAULT STREET: 1981 McGill College Avenue -
                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McGill University et al.
NVENTION: HUMAN AND MAMMALIAN DNA
1.8%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14;
; Pred. No.
  Score 14;
Pred. No.
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. 1.9e+03;
  DB 9; L
. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suite 1600
                 Length 30;
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Matches

14;

US-09-909-567B-35

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APPLICANT: Nair, Manoj
APPLICANT: Nair, Manoj
APPLICANT: Chen, Selyu
ITITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0214
CURRENT APPLICATION NUMBER: US/09/909,567B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/219,834
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic US-09-909-567B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 60, Applicati
Publication No. US2002
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.7%; Score 13; Best Local Similarity 100.0%; Pred. No. Matches 13; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 35, Application US/USY
Publication No. US20030022257A1
GENERAL INFORMATION:
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:

APPLICATION NUMBER: US/09/734,672
FILING DATE: 03-Dec-2000
PRIOR APPLICATION NATA:

APPLICATION NUMBER: US 08/966,436
FILING DATE: 07-NO. US20020183268A1-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 TITCATATTTTGTT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 TTTCATATTTTGTT 21
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Ave., N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Murphy, Patricia D. Allen, Antonette C.
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                        STATE: District of Columbia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09734672
No. US20020183268A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09909567B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Critz, Brenda S. Olson, Sheri J.
                                                                                                                                                                                                                                                                                                                                                                                                                                Schelter, Denise B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alvares, Christopher P.
                                                                                                                                                                                                                                                                                                                                                                                                                 Bin
                                                                                                                                                                                                                                                                                                                                                                           BRCA1 Gene
                                                                                                                                                                                                                                                                                                                                                                                          Coding Sequences of the Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-734-672-60
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US-09-982-828-60/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-739-3001 INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
        PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION UNMBER: US 09/074,453

FILING DATE: 1998-05-06

APPLICATION NUMBER: US 08/798,691

FILING DATE: 1997-02-12

APPLICATION NUMBER: US 08/598,591

FILING DATE: 1996-02-12

ATTORNEY,AGENT INFORMATION:

NAME: MICHAEL S.

NAME: MICHAEL S.

REFERENCE,DOCKET NUMBER: 44921-5053-01-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 GCTGGGAAAATGG 506
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                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/982,828
FILING DATE: 22-Oct-2001
CLASSIFICATION: (Unknown)
  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Avenue N. W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Coding Sequences of the Human BRCA1 Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Murphy, Patricia D.
Allen, Antonette C.
Alvares, Christopher P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Michael S. Tuscan
REGISTRATION NUMBER: 43,210
                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 20 base pairs
TYPE: nucleic acid
STRADDENNESS: No. US20020183268Al Relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12-Feb-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Critz, Brenda S. Olson, Sheri J. Thurber, Denise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bin
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Pred. No. 6.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/598,591
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RESULT 13 US-09-734-672-60/c

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RESULT 15
US-10-022-819-55/c
US-10-022-819-55/c
; Sequence 55, Application US/10022819
; Publication No. US20030027166A1
; GENERAL INFORMATION:
APPLICANT: ALLEN, Antonette C. P.
; APPLICANT: ALLEN, Antonette C. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN: 18R primer;
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-982-828-60
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Best Local Similarity 100.0%;
Matches 13; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-739-3000
TELEFAX: 202-739-3001
INFORMATION FOR SEO ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                            INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHRACTERISTICS:
SEQUENCE CHRACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/022,819
APPLICATION NUMBER: US/10/022,819
FILING DATE: 22-Apr-2002
CLASSIFICATION EXAMPLE (21-Apr-2002
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 09/074,452
FILING DATE: 1998-05-06
ATTORNEY/ACENT INFORMATION:
NAME: CUMKNOWN>
PRIOR APPLICATION TO THE PRIOR APPLICATION OF THE PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION STORMATION:
NAME: CUMKNOWN>
PRIOR APPLICATION TO THE PRIOR APPLICATION DATA:
APPLICATION STORMATION:
NAME: CUMKNOWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: 044921-5049-01-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-300
TELEFAX: 202-739-3001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAWRENCE, Tanmy
ANGELLY, Tracy S.

RABIN, Mark B.

TITLE OF INVENTION: CODING SEQUENCE HAPLOTYPE OF THE HUMAN
BRCAI GENE
NUMBER OF SEQUENCES: 67
                                                  HYPOTHETICAL: NO
                                                                   TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PRIMER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan Lewis & Bockius LLP
FRAGMENT TYPE: internal
                            ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: District of Columbia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1111 Pennsylvania Avenue CITY: Washington DC

 Mismatches

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; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-022-819-55
Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 494 GCTGGGAAAATGG 506
[|||||||||||||
Db 17 GCTGGGAAAATGG 5
Search completed: March 14, 2003, 10:59:22
Job time : 49.143 secs
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Result
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
   0 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on:
       989765482
                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq
   200220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OLIGO_NUC Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match
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780
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| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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       /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
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   ABK67133
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1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.9	1.9	1.9	1.9	1.9	1.9	2.1	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6
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22	22	22	22	22	21	20	20	22	22	22	22	22	21	21	21	21	21	16	22	20	22	24	21	17	21	21	21	21	21	21	21	21	21	21	21
AAC86405	AAC86403	AAC86402	AAF61241	AAH21118	AAZ44575	AAZ17990	AAZ17886	AAH61558	AAH61557	155	155	AAH61554	AAA86396	AAA86395	AAA86394	AAA86393		AAT25577	AAF76697	AAZ09965	AA164146	ABL40366	AAA96409	AAT16171	AAZ39088	AAZ39082	AAZ39081	AAZ39080	AAZ39079	AAZ39078	AAZ39077	AAZ39076		3907	AAZ39073
Human bc1-xL and b	Human bcl-xL and b	RNA	C. glutamicum tran		Newcastle disease	Homeobox conserved	RT-PCR primer spec	PCNA HH ribozyme b								PCBA HH ribozyme b	PCBA HH ribozyme b	gene	Human PTP1b coding	PTP1B forward PCR	Human PTBlB protei	Primer 2 relative	Primer used to amp	Primer #1 for huma	Human Al anti-apop	A1 ant	Human Al anti-apop	. ant	anti	Human Al anti-apop					

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#### ALIGNMENTS

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RESULT 1
ABK67134/c
ID ABK67134;
XX ABK67134;
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR prime
XX FY Primer; ss; DNA microarray; c
XX W POS-352829-B1.
XX W US6352829-B1.
XX PD 05-MAR-2002.
XX PD 05-MAR-2002.
XX PD 05-JAN-1999; 99US-0225928.
XX PD 05-MAY-1997; 97US-0859998.
XX PR 21-MAY-1997; 97US-0859998.
XX CCLON-) CLONTECH LAB INC.
XX PA (CLON-) CLONTECH LAB INC.
                                               Producing sub-population of labeled nucleic acids, useful for analysing differences in RNA profiles between several different physiological sources, using set of distinct gene specific primers –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer; ss; DNA microarray; differential expression analysis;
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RESULT 2
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Context the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at the printed specific and compare the patterns for each of the printed specification, but was obtained in electronic compared to context the context of the printed specific patterns and the patterns to context the sequence of the printed specific patterns and the patterns the sequence of the printed specific patterns and the pat
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Best Local
                                                Producing sub-population of labeled nucleic acids, useful for analysing differences in RNA profiles between several different physiological sources, using set of distinct gene specific primers
               Example 3;
                                                                                                                                                     WPI; 2002-314699/35
                                                                                                                                                                                                Chenchik A,
                                                                                                                                                                                                                                                                                                                                      05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2002 (first entry)
                                                                                                                                                                                                                                           (CLON-) CLONTECH LAB INC.
                                                                                                                                                                                                                                                                                           21-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer; ss; DNA microarray; differential expression analysis; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene specific PCR primer #1221.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 TCCGTAGACACTGCCAGAACACTATTCA 292
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                 SEQ
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                                                                                                                                                                                                                                                                                        97US-0859998
            ID No 1221; llpp; English
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Pred. No.
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RESULT 3
AAZ39089/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC The invention relates to producing a sub-population of labeled nucleic CC acids (NAs) comprising contacting a NA sample from a physiological CC source, with a pool of 50 distinct gene specific primers under suitable CC conditions to enzymatically generate sub-population of NAs, where CC each gene specific primer has a sequence complementary to a distinct CC MRNA, and each labeled NA is generated using a single gene specific CC NAS which is useful for analysing the differences in the RNA profiles CC between several different physiological sources, where the method CC comprises producing subpopulation of labeled NA sequence complementary to a distinct CC source to identify differences in the population, where the comparison CC is preferably performed by hybridising the population, where the comparison CC is preferably performed by hybridising the labeled NAs for each of the CC distinct physiological sources, to an array of probe NAs stably CC associated with the surface of a substrate to produce a hybridisation CC utilised in differential expression analysis of diseased a normal tissue of the sources, where differential gene expression assays are CC utilised in differential expression analysis of diseased a normal comparison content tissue of the printed specification, but was obtained in electronic CC Note: The sequence data for this patent did not form part CC in the printed specification, but was obtained in electronic CC format directly from USPTO at
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                Human; Al; anti-apoptotic; bcl-2-related protein; antisense inhibition; mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour; inflammation; diagnosis; phosphorothioate; PCR; probe; ss.
                                                                                                                                                                                                          07-JAN-1999;
                                                                                                                                                                                                                                           07-JAN-1999;
                                                                                                                                                                                                                                                                              14-DEC-1999
                                                                                                                                                                                                                                                                                                                US6001992-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Al anti-apoptotic bcl-2-related protein PCR probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ39089;
                                                                                                   WPI; 2000-061908/05
                                                                                                                                                                     (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ39089 standard; DNA; 22
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                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 TCCACCAGGCAGAAGATGACAGACTG
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26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 100.0%;
Conservative 0;
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                                                                                                                                    Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
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Example 9; Column 28; 28pp; English

Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis and treating associated diseases e.g. cancer -

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В Qy

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RESULT 4
AAT41123
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Best Local
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Primers T41001-T41382 are derived from novel human gene signature (GS) sequences which did not match with sequences deposited in Genbank release 76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins. The antisense oligonucleotides can be used as therapeutic agents to prevent or delay inflammation or tumour formation by promoting apoptosis in human cells or tissues. They can also be used as research agents to establish the function of particular genes and as diagnostic agents in sandwich assays for detecting the level of novel anti-apoptotic bcl-2-related proteins in a sample. The antisense oligonucleotides given in the present invention were designed to target human Al and mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The present sequence represents a PCR probe for the human Al nucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                       Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene signature HUMGS01288-derived sense primer.
                                                                                                                                                                                                                                                                                  Example 7; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ignature; messenger RNA; mRNA; relative abundance; frequency cloning; mapping; non-biased library; diagnosis; detection; yping; abnormal cell function; primer; PCR; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATSUBARA
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                                                                                                                                                                                                                                                                            7; 2245pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
0.79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Query Match Best Local Similarity

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Score 20; Pred. No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match-
                 Primers T41001-T41382 are derived from novel human gene signature (GS) sequences which did not match with sequences deposited in Genbank release 76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. The primers T41123-4 amplify clone pm2245 which comprises the GS HUMGS001288 (T20288), located on chromosome 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene signature; messenger RNA; mRNA; relative human; cloning; mapping; non-biased library; non-biased relation; primer;
                                                                                                                                                                                                                                                                      Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT41124 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as a means of diagnosing abnormal cell function or for recognising different cell types. The primers T41123-4 amplify clone pm2245 which comprises the GS HUMGS001288 (T20288), located on chromosome 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1995
                                                                                                                                                                                                                           Example 7; Fig 7; 2245pp;
                                                                                                                                                                                                                                                                                                                                      WPI; 1995-206931/27
                                                                                                                                                                                                                                                                                                                                                                   Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09514772-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT41124;
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                                                                                                                                                                                                                                                                                                                                                                                                  (OKUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       571 TGTGAAATGCTATCTCTCCT 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                  OKUBO
                                                                                                                                                                                                                                                                                                                                                                                                                 MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 BP; 4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                93JP-0355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-JP01916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMGS01288-derived anti-sense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 C; 3 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.6%;
                                                                                                                                                                                                                             Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relative abundance; frequency; library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amplification;
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                                                                                                                                                                                                                                                                                                    e.g.
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ACTGATATGGAAACGATTGC

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RESULT 7
AAZ39070/c
ID AAZ390
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AAZ39069/c
ID AAZ39069 standard; DNA; 20 BP.
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                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                             The present invention describes antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins. The antisense oligonucleotides can be used as therapeutic agents to prevent or delay inflammation or tumour formation by promoting apoptosis in human cells or tissues. They can also be used as research agents to establish the function of particular genes and as diagnostic agents in sandwich assays for detecting the level of novel anti-apoptotic bcl-2-related proteins in a sample. The antisense oligonucleotides
29-FEB-2000 (first entry)
                             AAZ39070;
                                                        AAZ39070 standard;
                                                                                                                                                                                                                                                                          given in the present invention were designed to target human Al and mcl-l anti-apoptotic bcl-2-related protein nucleotide sequences. The present sequence represents an antisense oligonucleotide for the human Al nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis and treating associated diseases e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Al; anti-apoptotic; bcl-2-related protein; antisense inhibition; mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour; inflammation; diagnosis; phosphorothloate; ss.
                                                                                                                                                                                                                                                Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ackermann EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JAN-1999;
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                                                                                                                                                            19 CATTGCCTCAACAGCTTCAA 38
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                                                                                                                                                                                         20;
                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                   2.6%;
                                                        DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                28pp; English.
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                                                                                                                                                                                       0;
                                                                                                                                                                                                      Score 20; DB 21;
Pred. No. 8.1;
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                                                                                                                                                                                                                 Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis and treating associated diseases e.g. cancer - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        071/c
AAZ39071 standard; DNA; 20
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mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                            inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Al anti-apoptotic bcl-2-related protein antisense oligo #17486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation; diagnosis; phosphorothicate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 GGTGAGCCAGCTCAAGACTT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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Matches 20
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                                                                                                                                                                                                                                                              Human;
mcl-l;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 given in the present invention were designed to target human {\tt Al} mcl-l anti-apoptotic bcl-2-related protein nucleotide sequences
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apoptosis; cancer; antiinflammatory; cytostatic; tumour;
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The present invention describes antisense oligonucleotides which the expression of novel anti-apoptotic bcl-2-related proteins. The antisense oligonucleotides can be used as therapeutic agents to gor delay inflammation or tumour formation by promoting apoptosis human cells or tissues. They can also be used as research agents establish the function of particular genes and as diagnostic agent
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Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bel-2-related proteins are useful for inducing apo and treating associated diseases e.g. cancer
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                                                                                                                                                                                  establish the function of particular genes and as diagnostic agents sandwich assays for detecting the level of novel anti-apoptotic bcl-2-related proteins in a sample. The antisense oligonucleotides given in the present invention were designed to target human Al and mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                   or delay inflammation or tumour formation by promoting apoptosis in human cells or tissues. They can also be used as research agents to
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ39074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 GCTGGCTCAGGACTATCTGC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGGCTCAGGACTATCTGC
                                                                                                                                                              anti-apoptotic bcl-2-related protein nucleotide sequences. in sequence represents an antisense oligonucleotide for the
                                                                                                                                          Al nucleotide sequence.
       20;
h 2.6%; Score 20; DB Similarity 100.0%; Pred. No. 8: 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity
                                                                                              20 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Column 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sis; cancer; antiinflammatory; cytostatic; tumour;
diagnosis; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marcusson EG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0226568
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                                                                                              Α;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                            4 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                       DB 21
8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
8.1;
                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dean
     0;
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                                           Length 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
0,
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  Gaps
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0;
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n

AAZ39076/c
ID AAZ39076 standard; DNA;
XX
XX
AC AAZ39076;
XX

20

ΒP

RESULT 13

밁 οy

20

GACACTGCCAGAACACTATT 1

271 GACACTGCCAGAACACTATT 290

Mismatches

0;

Indels

0; Gaps

0;

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RESULT 12
AAZ39075/c
ID AAZ390
XX AAZ390
XX AAZ390
XX 29-FEB
XX Uman;
KW Human;
KW Inflam
OS Synthe
OS Homo s
XX ITA
PD 14-DEC
XX ISIS-
PN 07-JAN
XX USSO01
XX WPI; 2
XX ANTISE
PT ANTISE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QY
   Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                    or delay inflammation or tumour formation by promoting apoptosis in human cells or tissues. They can also be used as research agents to establish the function of particular genes and as diagnostic agents sandwich assays for detecting the level of novel anti-apoptotic bel-2-related proteins in a sample. The antisense oligonucleotides given in the present invention were designed to target human Al and mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes antisense oligonucleotides which modulate the expression of novel anti-apoptotic bci-2-related proteins. The antisense oligonucleotides can be used as therapeutic agents to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins are useful for inducing apo and treating associated diseases e.g. cancer -
                                                                                                                             Sequence
                                                                                                                                                                                            present sequence represents an antisense oligonucleotide for the human Al nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 21; Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-061908/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Al anti-apoptotic bcl-2-related protein antisense oligo #17490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ39075 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ackermann EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ39075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation; diagnosis; phosphorothioate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGTTGCGTTCTCAGTCCA 212
   l Similarity
20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptosis; cancer; antiinflammatory; cytostatic;
mation; diagnosis; phosphorothicate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Al; anti-apoptotic; bcl-2-related protein; antisense inhibition;
                                                                                                                             20 BP; 4 A; 3 C; 6 G; 7 T; 0 other;
2.6%; S ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0226568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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                                  Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bennett CF,
                           No.
                                                                  DB 21;
                                  8.1;
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                                                              Length 20;
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RESULT 14
AAZ39077/c
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes antisense oligonucleotides which most the expression of novel anti-apoptotic bcl-2-related proteins. The antisense oligonucleotides can be used as therapeutic agents to prevail of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bcl-2 related proteins in a sample. The antisense oligonucleotides given in the present invention were designed to target human Al and mcl-l anti-apoptotic bcl-2-related protein nucleotide sequences. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis and treating associated diseases e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6001992-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 21; Column 27; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Al; anti-apoptoric; bcl-2-related protein; antismed-1; apoptosis; cancer; antiinflammatory; cytostatic; inflammation; diagnosis; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
US6001992-A
                                                                                             Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
                                                                                                                                                                                                                                               AAZ39077 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-FEB-2000
                                               Synthetic
                                                                                                                                               Human Al anti-apoptotic bcl-2-related protein antisense oligo #17492.
                                                                                                                                                                                29-FEB-2000
                               Homo sapiens
                                                                                inflammation;
                                                                                                                                                                                                                                                                                                                                                               309 GGAGTTTGAAGACGGCATCA 328
                                                                                                                                                                                                                                                                                                                                 20 GGAGTTTGAAGACGCCATCA 1
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-061908/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
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nilarity 100.0%;
Conservative 0
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                                                                                                                                                                                (first entry)
                                                                               diagnosis; phosphorothicate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 C; 3 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EG,
                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
. 8.1;
                                                                                SS
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
AA239078/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 21; Column 27; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ackermann EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JAN-1999;
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WPI; 2000-061908/05
                                 Ackermann EJ, Marcusson
                                                                                                 07-JAN-1999;
                                                                                                                                  07-JAN-1999;
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                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                   29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ39078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ39078 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 3 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS
                                                                (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 AAGAAACTTCTACGACAGCA 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                  PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 C; 5 G;
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                                  EG,
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establish the function of particular genes and as diagnostic agents sandwich assays for detecting the level of novel anti-apoptotic bcl-2-related proteins in a sample. The antisense oligonucleotides given in the present invention were designed to target human Al and mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The present sequence represents an antisense oligonucleotide for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition; mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour; inflammation; diagnosis; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antisense oligonucleotides can be used as therapeutic agents to prevor delay inflammation or tumour formation by promoting apoptosis in human cells or tissues. They can also be used as research agents to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and treating associated diseases e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Al anti-apoptotic bcl-2-related protein antisense oligo #17493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20;
Pred. No.
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Bennett
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CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
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Ax Antisense oligonucleotides which modulate the expression of novel pr and treating associated diseases e.g. cancer - XX

Claim 21; Column 27; 28pp; English.

XX

Claim 21; Column 27; 28pp; English.

XX

Crime present invention describes antisense oligonucleotides which modulate CC the expression of novel anti-apoptotic bcl-2-related proteins. The CC antisense oligonucleotides can be used as therapeutic agents to prevent CC or delay inflammation or tumour formation by promoting apoptosis in CC bundan cells or tissues. They can also be used as research agents to cc establish the function of particular genes and as diagnostic agents in CC sandwich assays for detecting the level of novel anti-apoptotic cc cc l-2-related proteins in a sample. The antisense oligonucleotides can be used as research agents in CC given in the present invention were designed to target human Al and CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The present sequence represents an antisense oligonucleotide for the present sequence.

SQ Sequence 20 Bp; 5 A; 6 C; 2 G; 7 T; 0 other;

Ouery Match

Description of particular sequence of the collection o
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Run

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Minimum DB
Maximum DB
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780
24791104 seqs, 12571243825 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/pna/US102B_COMB
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/ Cgn2_6/ptodata/1/pna/US6006_COMB.seq:
/ Cgn2_6/ptodata/1/pna/US6000_COMB.seq:
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/ Cgn2_6/ptodata/1/pna/US6023_COMB.seq:
/ Cgn2_6/ptodata/1/pna/US6032_COMB.seq:
/ Cgn2_6/ptodata/1/pna/US6034_COMB.seq:
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/cgn2_6/ptodata/1/pna/US6001_COMB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

1 PCT-US99-2953-13
1 PCT-US99-2953-14
1 PCT-US99-2953-16
1 PCT-US99-2953-16
3 US-09-869-894-2
33 US-09-869-894-3
33 US-09-869-894-7
33 US-09-869-894-7
33 US-09-869-894-7
33 US-09-869-894-7
33 US-09-869-894-10
33 US-09-869-894-11
34 US-09-869-894-11
35 US-09-869-894-12
36 US-09-869-894-12
37 US-09-869-894-15
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34 US-09-869-894-16
35 US-09-869-894-16
36 US-09-969-894-16
37 US-09-969-894-16

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Sequence 28, Appl
Sequence 36231, A
Sequence 36231, A
Sequence 70874, A
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Sequence 15, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 10, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appli
Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
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Sequence 18, Appl
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Sequence 15,
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APPLICANT: Pry, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMM
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMM
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMM
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMM
TITLE OF INVENTION: METHODS INFLAMMATORY DISEASES
FILE REFERENCE: 5061200120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT APPLICA
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APPLICANT: Altman, Peter
TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
FILE REFERENCE: 50661200140
CURRENT APPLICATION NUMBER: PT/US01/47856
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/241,994
PRIOR APPLICATION NUMBER: US 60/241,994
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION UNMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 8832
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3838
LENGTH: 50
                              RESULT 4
US-10-131-827-3838
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US-10-131-827-2596
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Sequence 3838, Application US/10131827
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Best Local S
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                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity 100.0%; Pred. No. 7.7e-16;
Matches 50; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                     703 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                703 TIGATGATGTAACTIGACCTICCAGAGTIATGGAAATTITGTCCCCCATGT 752
                                                                                                                                                                     1 TIGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 50
                                                                                                                                                                                                                                                                                                             Local Similarity 100.0%; nes 50; Conservative 0;
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Phillips, Julie
Woodward, Robert
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Quertermous, Thomas
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                                                                                                                                                                                                                                                                                                     6.4%; Score 50; DB 40; L
100.0%; Pred. No. 7.7e-16;
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APPLICANT: Johnson, Frances
APPLICANT: Fry, Kirk
APPLICANT: Matcuk, George
APPLICANT: Matcuk, George
APPLICANT: Prentice, James
APPLICANT: Philips, Julie
APPLICANT: Philips, Julie
APPLICANT: APPLICANT: Philips, Julie
APPLICANT: APPLICANT: Altman, Peter
TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
CURRENT APPLICATION NUMBER: PCT/USO1/47856
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/241,994
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/241,994
PRIOR FILING DATE: 2000-16-08
NUMBER OF SEQ ID NOS: 8832
SOFTWARE: Patentin version 3.1
SEQ ID NO 2596
LENGTH: 50
TYPER: DNA

PCT-US01-47856-2596

Sequence 2596, Application PC/TUS0147856 GENERAL INFORMATION:

ALIGNMENTS

INFORMATION

APPLICANT: BIOCARDIA, INC.
APPLICANT: Wohlgemuth, Ja
APPLICANT: Quertermous, J

Wohlgemuth, Jay Quertermous, Thomas

PCT-US01-47856-3838 : Sequence 3838, Application PC/TUS0147856 ; GENERAL INFORMATION:

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; ORGANISM: Homo sapiens PCT-US01-47856-2596

Query Match 6.4%; So Best Local Similarity 100.0%; F Matches 50; Conservative 0;

Score 50; DB 1; Le; Pred. No. 7.7e-16; 0; Mismatches 0;

Length 50; Indels

RESULT 2

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; SEQ ID NO 2596
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-2596
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                                                                                                                      RESULT 6
US-10-131-831-3838
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NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3838
LENGTH: 50
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 50; Conserv
                  Sequence 3838, Application US/10131831
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2596, Application US/10131831 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 10/006,290 PRIOR FILING DATE: 2001-10-22 PRIOR APPLICATION NUMBER: US 60/296,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TITLE REFERENCE: 506612000120
TILE REFERENCE: 506612000120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
TITLE OF INVENTION: TRANSPLANT REJECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/131,827 CURRENT FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 10/006,290 PRIOR FILING DATE: 2001-10-22 PRIOR APPLICATION NUMBER: US 60/296,764
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
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1 TIGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT 50
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Woodward, Robert
                                                                                                                                                                                                                                                                                               6.4%; So illarity 100.0%; I Conservative 0;
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OTHER INFORMATION: oligonucleotide primer; SEQUENCE DESCRIPTION: SEQ ID NO: 1222: US-09-225-201B-1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1222, Application US/09225201B
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.4%;
Best Local Similarity 100.0%;
Matches 50; Conservative (
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CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TITLE OF INVENTION: TRANSPLANT REJECTION FILE REFERENCE: 506612000121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEPAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1222:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           703 TTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: WINDOWS95
SOFTWARE: FastSEQ for Window
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: U5/08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: F161d, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bibilashvilli, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
                                                                   FEATURE:
                                                                                        MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/225,201B FILING DATE: 05-Jan-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2200 San
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
                                                                                                             TOPOLOGY:
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PCT-US99-29593-17/c 
; Sequence 17, Application PC/TUS9929593 
; GENERAL INFORMATION:
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                                                                                          RESULT 9
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; Sequence 1221, Application US/09225201B
; GENERAL INFORMATION:
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Best Local
APPLICANT: Ackermann, Elizabeth J. APPLICANT: Bennett, C. Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-854-0875 INFORMATION FOR SEQ ID NO: 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 TCCGTAGACACTGCCAGAACACTATTCA 292
                                                                                                                                                                         64 TCCACCAGGCAGAAGATGACAGACTG 89
                                                                                                                                                                                                            Local Similarity
les 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chenchik, Alex
Jokhadze, George
                                                                                                                                       TCCACCAGGCAGAAGATGACAGACTG 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
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28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/225,201B
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
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Pred. No.
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0.011;
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RESULT 11
PCT-US99-29593-2/c
; Sequence 2, Application PC/TUS9929593; GENERAL INFORMATION:
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Matches
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CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 09/226,568
PRIOR FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/09869894 GENERAL INFORMATION:
               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                      Query Match
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NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ackermann, APPLICANT: Bennett,
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APPLICANT: Marcusson, Eric G.
APPLICANT: Isis Pharmaceuticals, Inc.
TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bc1-2-related
TITLE OF INVENTION: Proteins
FILE REFERENCE: ISPH-0432
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CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 09/226,568
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                ACGATTGCCAACACATACTTCT 1
                               Ackermann, Elizabeth J. Bennett, C. Frank Dean, Nicholas M.
Marcusson, Eric G.
Isis Pharmaceuticals, Inc.
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Isis Pharmaceuticals, Inc.
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Pred. No.
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APPLICANT:

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PCT-US99-29593-3
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PCT-US99-29593-3/c
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CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 09/226,568
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
                                                                                                                                                      Sequence 4, Application PC/TUS9929593 GENERAL INFORMATION:
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Best Local
           APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Isis Pharmaceuttcals, Inc.
TITLE OF INVENTION: Antisense Modulation
TITLE OF INVENTION: Proteins
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CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 09/226,568
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related TITLE OF INVENTION: Proteins
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REFERENCE:
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CURRENT APPLICATION NUMBER: PCT/US99/29593
CURRENT FILING DATE: 1999-12-14
EARLLER APPLICATION NUMBER: 09/226,568
EARLLER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 40
SOFTMARE: PatentIN Ver. 2.0
SEQ ID NO 5
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                         Sequence 6, Application PC/TUS9929593
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Isis Pharmaceuticals, Inc.
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Matches 20
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GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
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CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 09/226,568
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 4
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Best Local Similarity 100.0%;
Matches 20; Conservative
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TITLE OF INVENTION: Antisense modulation of TITLE OF INVENTION: Proteins FILE REFERENCE: ISSH-0432 PCT/US99/29593 CURRENT APPLICATION UMBER: PCT/US99/29593 EARLIER APPLICATION NUMBER: 09/226,568
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TYPE: DNA
ORGANISM: Artificial Sequence
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EARLIER FILING DATE: 1999-01-07

NUMBER OF SEQ ID NOS: 40

SED ID NO 6

LENGTH: 20

TYPE: DNA

OBGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-6

Query Match
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Gaps 0;

MINIMITATION DESCRIPTION DESCR
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

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3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

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7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	% Query Match	Length DB	ID	Description
1	50	6.4	50 8	US-10-325-899-2596	Sequence 2596, Ap
2	50	6.4		US-10-325-899-3838	3838,
w	22	2.8	25	US-60-427-836-533438	533438
c 4	21	2.7	21 8	US-10-310-188-73875	
ი 5	19			Us-10-310-188-85737	85737,
6	19			US-60-427-836-6872	6872, F
7	18			US-60-427-836-59598	59598,
8	17	2.2		US-60-427-808-360861	
	17			US-60-427-808-757664	
c 10	16			US-10-303-778-10504	
	16			US-10-355-577-67556	
12	16			US-10-355-577-149144	149144,
13	16	2.1	_	US-10-355-577-249093	
14	16	2.1		US-10-355-577-317546	Sequence 317546,
c 15	16	2.1		US-10-355-577-487471	
	16	2.1		us-10-355-577-535019	
c 17	16	2.1	25 9	US-60-427-808-272157	Sequence 272157,
	16	2.1		US-60-427-808-415756	Sequence 415756,
c 19	16	2.1		US-60-427-808-595802	
20	16	2.1		US-60-427-808-730126	
c 21	16	2.1	25 9	US-60-427-808-875365	
c 22	16	2.1	25 9	US-60-427-836-238638	
23	16	2.1	25 9	US-60-427-836-242560	
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RESULT 1 Sequence 25 GENERAL INF GENERAL INF APPLICANT:		22222222222222222222222222222222222222
SULT 1  Sequence 2596, Applica GENERAL INFORMATION: APPLICANT: Wohlgemuth APPLICANT: Ly, Nick APPLICANT: Woodward, TITLE OF INVENTION: FILLE REFERENCE: 50661 CURRENT FILING DATE: PRIOR APPLICATION NUD PRIOR APPLICATION NUD PRIOR FILING DATE: 2C PRIOR FILING DATE: 3C PRIOR FILING DATE:		555555555555555555555555555555555555555
ULT 1 10-325-899-2596 10-325-899-2596 equence 2596, Application US/10 EMERAL INFORMATION: APPLICANT: Wohlgemuth, Jay APPLICANT: Wohlgemuth, Jay APPLICANT: Woodward, Robert TITLE OF INVENTION: METHODS AND TITLE OF INVENTION: METHODS AND TITLE OF INVENTION RELECTION FILE REFERENCE: 506612000122 CURRENT APPLICATION NUMBER: US/ CURRENT FILING DATE: 2002-12-2 PRIOR APPLICATION NUMBER: US 60, PRIOR TILING DATE: 2001-06-08 PRIOR APPLICATION NUMBER: US 10, PRIOR FILING DATE: 2001-0-22 PRIOR APPLICATION NUMBER: US 10, PRIOR FILING DATE: 2002-04-24 UMBER OF SEQ 1D NOS: 9966		
ccation US/103 rth, Jay rtk oc od, Robert METHODS AND REJECTION 161200122 rUMBER: US/1 12002-12-2 12001-06-08 12001-06-08 12001-10-2 1001BER: US 10/ 2001-10-2 1001BER: US 10/ 2001-04-24 1S: 9966		00000000000000000000000000000000000000
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325899 COMPOSITIONS FOR 10/325,899 0 /296,764 /006,290 /131,831	ALIGNMENTS	PCT-1L02-00722-5 US-10-098-2639-25291 US-10-098-2639-202039 US-10-355-577-2912 US-10-355-577-2915 US-10-355-577-51855 US-10-355-577-405610 US-10-355-577-406613 US-10-355-577-406011 US-10-355-577-406011 US-10-355-577-406011 US-10-355-577-406011 US-10-355-577-934208 US-60-417-190-3450 US-60-417-190-3450 US-60-417-190-3450 US-60-427-808-138267 US-60-427-808-1333996 US-60-427-808-333996 US-60-427-808-333996
DlagNOSING AND M		sequence sequence
MONITORING		5, App11 55,912, Ap 92039, A 2912, Ap 29125, Ap 51855, A 4615737, 461585, 708610, 718610, 74861, 842893, 93,408, 93,408, 945, App 3450, App
TRANSPI		

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PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-66-08
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 9966
SOFTWARE: Patentin version 3.1
SEQ ID NO 3838
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-325-899-3838
                                                                   TITLE OF INVENTION: BIGINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILL REFREENCE: 47487
CURRENT PEPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID MOS: 86481
SOFTMARE: Patentin version 3.1
SEG ID NO 73875
LENGTH: 21
TYPE: DNA
CORGANIZM: Homo Sapiens
US-10-310-188-73875
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US-10-310-188-73875/c
Sequence 73875, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROSettaGemonics
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; ORGANISM: Rattus norvegicus
US-60-427-836-533438
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US-60-427-836-533438
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CURRENT APPLICATION NUMBER: US/60/427,836
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEO ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEO ID NO 533438
LENGTH: 25
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APPLICANT: Xue Mei Zhou
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Best Local Similarity
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                   Best
                                 Query Match
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CURRENT FILING DATE: 2002-12-20
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 Local Similarity les 21; Conserva
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2.7%;
ilarity 100.0%;
Conservative
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                 score 21; DB 8;
pred. No. 0.8;
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CURRENT APPLICATION NUMBER: US/60/427,836
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699465
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 6872
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-60-427-836-6872
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US-60-427-836-6872
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US-10-310-188-85737/c
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                            Sequence 59598, Application US/60427836
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527
CURRENT APPLICATION NUMBER: US/60/427,836
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 59598
LENGTH: 25
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CURRENT FILING DATE: 2002-12-19
NUMBER OF SED ID NOS: 88841
SOFTWARE: Patentin version 3.1
SED ID NO 85737
LENGTH: 19
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GENERAL INFORMATION:
APPLICANT: ROSettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY (
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
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GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of
FILE REFERENCE: 3527
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Best Local Similarity
Matches 19; Conserv
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Best Local
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ORGANISM: Rattus norvegicus
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RESULT 10

RESULT 10

US-10-303-778-10504/c

Sequence 10504, Application US/10303778

GENERAL INFORMATION:
APPLICANT: ROSettaGenomics

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF ITILE OF INVENTION: REGULATORY GENES AND USES THEREOF FILE REFERENCE: 47416

CURRENT APPLICATION NUMBER: US/10/303,778

TIDDENT FILING DATE: 2002-11-26
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US-60-427-808-757664/c
Sequence 757664, Application US/60427808
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis
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US-60-427-808-360861
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528
CURRENT APPLICATION NUMBER: US/60/427,808
CURRENT ELLING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 360861
ENERTH: 25
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Best Local S
Matches 18
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CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 757664
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nes 17; Conserv
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ilarity 100.0%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 0;
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Pred. No.
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; SEQ ID NO 10504
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Infectious h
US-10-303-778-10504
                                                                                                               CURRENT APPLICATION NUMBER: US/10/355,577
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOPTWARE: Microarray Probe Sequence Listing Generator V :
SEQ ID NO 149144
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-355-577-149144
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CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SEQ ID NO 67556
LENGTH: 25
TYPE: DNA
CRGANIZSM: Homo sapien
US-10-355-577-67556
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GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3121
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GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3121
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Best Local :
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SOFTWARE: PatentIn version 3.1
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                            380 AGAAACTTCTACGACA 395
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; Pred. No. 4.3e+02
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RESULT 13
US-10-355-577-249093
; Sequence 249093, Application US/10355577
; GENERAL INFORMATION:

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US-10-355-577-487471/c
US-10-355-577-487471/c
Sequence 487471, Application US/10355577
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-Ul33
FILE REFERENCE: 3121
                                                                                                                                                                  ; ORGANISM: Homo sapien US-10-355-577-487471
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US-10-355-577-317546
Sequence 317546, Application US/10355577
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
APPLICANT: MITTMANN, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-Ul33
FILE REFERENCE: 3121
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CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 4874/1
LENCTH: 25
TYPE: DNA
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Best Local S
Matches 16
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CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 31746
LENGTH: 25
LENGTH: 25
TYPE: DNA
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CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID 0249993
LENGTH: 25
TYPE: DNA
TYPE: DNA
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TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-Ul33
FILE REFERENCE: 3121
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Local Similarity 100.0%; Pred. No. 4.3e+02;
nes 16; Conservative 0; Mismatches 0; Indels
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ACCAGAAAGGACACTC 6
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#### REFERENCE AUTHORS TITLE JOURNAL FEATURES RESULT 1 186713/c LOCUS DEFINITION SOURCE ORGANISM ACCESSION VERSION Result No. KEYWORDS C 000000 00000 000000000000000000000000 Score Sequence 186713 186713.1 1 (bases 1 to 21) Reed, J.C. and Sato, T. Interaction of proteins involved in a cell Patent: US 5702897-A 1 30-DEC-1997; Location/Qualifiers Unclassified. Unknown Unknown Query Match 1 from patent Length 18675066 AR095066 AR095066 AR095069 AR095070 AR095070 AR095077 AR095077 AR095077 AR095077 AR095077 AR095082 AR095082 AR095084 AR095085 AR095085 AR095086 AR095086 AR095087 AR095087 AR095088 AR0888 AR0888 AR0888 AR0888 AR0888 AR0888 AR08883 AR236883 IJ $s_0$ ALIGNMENTS SUMMARIES 21 bp 5702897. DNA linear A20477 oligonucleo AX250150 Sequence 18678 Sequence 1 AX009974 Sequence AX236902 Sequence AX236902 Sequence AX239779 Sequence AX239779 Sequence AX136905 Sequence AX136052 Sequence AR095066 Sequence AR095068 Sequence AR095069 Sequence AR095070 Sequence AR095071 Sequence AR095071 Sequence AR095072 Sequence AR095073 Sequence AR095074 Sequence AR095075 Sequence AR095076 Sequence AR095076 Sequence AR095077 Sequence AR095078 Sequence AR095078 Sequence AR095081 Sequence AR095081 Sequence AR095082 Sequence AR095083 Sequence AR095084 Sequence AR095085 Sequence AR095085 Sequence AR095086 Sequence AR095086 Sequence AR095087 Sequence AR095087 Sequence AR095088 Sequence AR095087 Sequence AR165304 AX488272 Description PAT Sequence 1 (04 Sequence ?72 Sequence 47 Sequence 59 Sequence 61 Sequence 10-JUN-1998

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Ackermann, E. J., Bennett, C. Frank., Dean, N.M. and Marcusson, E. Antisense modulation of novel anti-apoptotic bcl-2-related patent: US 6001992-A 20 14-DEC-1999;
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Ackermann, E.J., Bennett, C. Frank., Dean, N.M. and Marcusson, E.G.
Antisense modulation of novel anti-apoptotic bcl-2-related proteins
Patent: US 6001992-A 19 14-DEC-1999;
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Sequence
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' 'bases 1 to 20)
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AR095068
                   1 (bases 1 to 20)
Ackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, E.G.
Antisense modulation of novel anti-apoptotic bcl-2-related propatent: US 6001992-A 23 14-DEC-1999;
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Ackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, E.G.
Antisense modulation of novel anti-apoptotic bcl-2-related pro
Patent: US 6001992-A 22 14-DEC-1999;
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Sequence
AR095072
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1 (bases 1 to 20)
Ackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, E. Antisense modulation of novel anti-apoptotic bc1-2-related patent: US 6001992-A 25 14-DEC-1999;
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20; Conserv
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Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
Antisense modulation of novel anti-apoptotic bcl-2-related proteins
Patent: US 6001992-A 24 14-DEC-1999;
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AR095074/c
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1 (bases:1 to 20)

Ackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, E.G. Antisense modulation of novel anti-apoptotic bcl-2-related propatent: US 6001992-A 26 14-DEC-1999;
                                                                  Unknown.
Unknown.
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Ackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, 1
Antisense modulation of novel anti-apoptotic bcl-2-related
Patent: US 6001992-A 27 14-DEC-1999;
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         1 (bases 1 to 20)
Ackermann, E.J., Bennett, C.Frank., Dean, N.M. a
Antisense modulation of novel anti-apoptotic
Patent: US 6001992-A 28 14-DEC-1999;
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Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
Antisense modulation of novel anti-apoptotic bcl-2-related proteins
Patent: US 6001992-A 30 14-DEC-1999;
Location/Qualifiers
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Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
Antisense modulation of novel anti-apoptotic bcl-2-related proteins
Patent: US 6001992-A 29 14-DEC-1999;
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AR095076
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AR095079
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Ackermann, E.J., Bennett, C.Frank., Dean, N.M. and Marcusson, E.G.
Antisense modulation of novel anti-apoptotic bcl-2-related propatent: US 6001992-A 32 14-DEC-1999;
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1 (bases I to 20)

Ackermann, E.J., Bennett, C. Frank., Dean, N.M. and Marcusson, E.G.

Antisense modulation of novel anti-apoptotic bcl-2-related proteins Patent: US 6001992-A 112.
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  WPI; 2001-343812/36
                                                                                                                                                                                                                          Human Mc1-1 DNA extending PCR primer, #105C.
                    Craig RW,
                                                                              14-JAN-2000; 2000WO-US00969
                                                                                                25-MAY-2001.
                                                                                                                    WO200136594-A1
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           AAT03164-T031366 are primers used for the amplification of the hum Mc1-1 gene. The Mc1-1 protein is a Bc1-2 related protein, the Mc1-protein was expressed and used to investigate the interactions of Mc1-1 with other proteins known to be involved in apoptosis (excluding the Bax protein). Proteins detected using this method (excluding the Bax protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to Mc1-1 gene regulatory elements and the variant Mc1-1s/deltaTM. The anti-apoptotic Mc1-1 protein is encoded by exons 1, 2 and 3. The pro-apoptotic Mc1-1s/DeltaTM variant encoded by exons 1 and 3 is obtained due to alternative mRNA splicing. The Mc1-1 gene regulatory element is useful for modulating the Mc1-1 gene expression in a cell e.g., neuronal cell or tumour cell, such that apoptosis of the cell is induced or cell viability is increased. The Mc1-1 and its regulatory elements are used for treating pathological conditions which include cancer, diabetic retinopathy, corneal graft conditions which include cancer, diabetic retinopathy, corneal graft neovascularisation and neovascular glaucoma, epithelial conditions such as psoriasis, autoimmune diseases like rheumatoid arthritis, systemic lupus erythematosus, and neurodegenerative diseases. The present sequence is a PCR primer #105c, used for the extension reaction of the human
                                                                                                       Example 1; Page 22; 62pp; English.
                                                                                                                                    Detection of novel proteins involved in apoptosis - with proteins involved in apoptosis
                                                                                                                                                                                  WPI; 1995-373811/48
                                                                                                                                                                                                                                                                                                         12-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                  WO9528497-AL
                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                           detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Mcl-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Mcl-1 gene regulatory elements, useful for modulating expression of Mcl-1 polypeptide or its variant which regulate apoptosis in neuronal or tumor cells -
                                                                                                                                                                                                                                             (LJOL-) LA JOLLA CANCER RES FOUND
                                                                                                                                                                                                                                                                           13-APR-1994;
                                                                                                                                                                                                                                                                                                                                     26-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mcl-1; Bax; apoptOsis; cell death; regulation; Bcl-2; novel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT03164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT03164 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30 BP; 7 A; 9 C; 8 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
upstream activators or downstream effectors of a cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene first strand primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                Τ;
                                                                                                                                                                                                                                                                           94US-0226876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22,
5. 0.00072;
0;
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             this method car
                                                                                                                                                   interaction
                                                          the Mcl-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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AAX26538
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                                                                                                                                                                RESULT 4
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Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                              specification describes methods for DNA amplification, wherein a template DNA containing nucleotide analogues is amplified in the presence of nucleotide analogues and a substance which lowers the Tm value of double-stranded nucleic acids. Suitable nucleotide analogues are 7-deaza-dGTP, 7-deaza-dATP, dITP and hydroxymethyl-dGTP. Suitable Tm value-lowering substances are formamide, dimethyl sulphoxide and trimethylgiycine. The methods improve the amplification of DNA. Also, DNA fragments which originated as RNA can be amplified without particular the particular of the property of the substance of the careful of the control of the control of the careful of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simple and accurate method for DNA amplification – uses amplification in the presence of nucleotide analogues together with a compound which lowers the Tm of double-stranded nucleic acids {\tt acc}
                                                                                                                                                                                                                                                                                                Sequence 21 BP; 4 A; 5 C; 7 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                          purifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primers AAX26538-39 were used to exemplify the invention. specification describes methods for DNA amplification, wherei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-181059/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hino F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-1997;
14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1235 GCAAGTGGCAAGAGGATTATG 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein such as Bax which induces apoptosis. If the protein Bcl-2 related protein apoptosis levels are decreased due to protein binding to and inactivating Bax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 31; 36pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09909213-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA amplification; nucleotide analogue; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer P12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX26538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 4 A; 8 C; 2 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX26538 standard;
                                                                     586 CGGCAGTCGCTGGAGATTATC 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-AUG-1998;
                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GCAAGTGGCAAGAGGATTATG 1
    CGGCAGTCGCTGGAGATTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kato I,
                                                                                                                                                                                                                                                                                                                                                                     the RNAs in sample.
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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97JP-0231885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mukai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                              0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
21
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                                                                                                                                                                                Score 21;
Pred. No.
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Pred. No.
                                                                                                                                                Mismatches
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                                                                                                                                                                                DB 20;
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                                                                                                                                                0,
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                                                                                                                                                                                                                     Length 21;
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                                                                                                                                           Indels
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                                                                                                                                           Gaps
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                                                                                                                                                      RESULT
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Best Local
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                                                                                                                                                                                                                                                                                   specification describes methods for DNA amplification, wherein a template DNA containing nucleotide analogues is amplified in the presence of nucleotide analogues and a substance which lowers the Tm value of double-stranded nucleic acids. Suitable nucleotide analogues are 7-deaza-dGTP, 7-deaza-dATP, dTTP and hydroxymethyl-dUTP. Suitable Tm value-lowering substances are formamide, dimethyl sulphoxide and trimethylgycine. The methods improve the amplification of DNA. Also, DNA fragments which originated as RNA can be amplified without more than the DNA.
                  Human; Mcl-1 gene regulatory element; Mcl-1s/deltaTM variant; neuronal cell; tumour cell; apoptosis; therapy; cancer; psoriasis; diabetic retinopathy; corneal graft neovascularisation; neovascular glaucoma; epithelial condition; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
                                                                                                                                                                                                   1014 CTTCCATGTAGAGGACCTAGA 1034
                                                                                                                                                                                                                                                                                                                                                                                                     Simple and accurate method for DNA amplification - uses amplification in the presence of nucleotide analogues together with a compound which lowers the Tm of double-stranded nucleic acids
          neurodegenerative
                                                                         Human Mcl-1 cDNA amplifying RT-PCR primer, Mcl-1-F5
                                                                                              10-AUG-2001
                                                                                                                                                                                                                                                          Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-OCT-1997;
14-AUG-1997;
                                                                                                                                  AAD06439 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                  PCR primers AAX26538-39 were used to exemplify the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-181059/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TAKI ) TAKARA SHUZO CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA amplification; nucleotide analogue; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer P13
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                                                                                                                                                                                 CTTCCATGTAGAGGACCTAGA 1
                                                                                                                                                                                                                                                                                                                                                                                      6;
                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                              the RNAs in sample.
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                            (first entry)
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97JP-0231885.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mukai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                    36pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                               0.5%;
                                                                                                                                   21
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       PCR primer;
                                                                                                                                   ΒP
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                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                               Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto
                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                     RESULT 6
AAD06441/c
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Best Local :
                                                                                                                                                                                                                                                                                                Matches
       14-JAN-2000; 2000WO-US00969.
                                                               Ното
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Mcl-1 gene regulatory of Mcl-1 polypeptide or its neuronal or tumor cells -
                                           WO200136594-A1
                                                                                                                                                                                                          AAD06441 standard;
                          25-MAY-2001
                                                                                 neurodegenerative
                                                                                                                                                                     10-AUG-2001
                                                                                                                                                                                        AAD06441;
                                                                                                                                                                                                                                                                                                                                   Sequence 21
                                                                                                                                                                                                                                                                                                                                                       Mcl-1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-343812/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200136594-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DART-) DARTMOUTH COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-1999;
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                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                          5 GTAAGGAGTCGGGGTCTTCCC
                                                               sapiens
                                                                                                                                                 Mcl-1 cDNA amplifying RT-PCR primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RW,
                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 75; 125pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bingle CD,
                                                                                                                                                                                                                                                                                                                                    BP; 3 A;
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                      0.5%;
                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                   5 C; 8 G;
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                                                                                                                                                                                                                                                                           25
                                                                                PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                       Score 21;
Pred. No.
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17;
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The present invention relates to Mcl-1 gene regulatory elements and the variant Mcl-1s/deltaTM. The anti-apoptotic Mcl-1 protein is encoded by exons 1, 2 and 3 The pro-apoptotic Mcl-1s/DeltaTM variant encoded by exons 1 and 3 is obtained due to alternative mRNA splicing. The Mcl-1 gene expression in a cell e.g., neuronal cell or tumour cell, such that apoptosis of the cell is induced or cell vlability is increased. The Mcl-1 and its regulatory elements are used for treating pathological conditions which include cancer, diabetic retinopathy, corneal graft neovascularisation and neovascular glaucoma, epithelial conditions such as psoriasis, autoimmune diseases like Theumatoid arthritis, systemic lugus erythematosus, and neurodegenerative diseases. The present sequence is a RT-PCR primer Mcl-1-F5, used for the amplification of the human
                                Human; Mcl-1 gene regulatory element; Mcl-1s/deltaTM variant; neuronal cell; tumour cell; apoptosis; therapy; cancer; psorias diabetic retinopathy; corneal graft neovascularisation; neovascular glaucoma; epithelial condition; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
tis; systemic lupus erythematosus;
disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  elements, useful for modulating expression variant which regulate apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                           Mcl-1-R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                         cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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16-NOV-1999;

99US-0166113

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to Mc1-1 gene regulatory elements and the variant Mc1-1s/deltaTM. The anti-apoptotic Mc1-1 protein is encoded by exons 1, 2 and 3. The pro-apoptotic Mc1-1s/DeltaTM variant encoded by exons 1 and 3 is obtained due to alternative mRNA splicing. The Mc1-1 gene regulatory element is useful for modulating the Mc1-1 gene expression in a cell e.g., neuronal cell or tumour cell, such that apoptosis of the cell is induced or cell viability is increased. The Mc1-1 and its regulatory elements are used for treating pathological conditions which include cancer, diabetic retinopathy, corneal graft neovascularisation and neovascular glacucoma, epithelial conditions such as psoriasis, autoimmune diseases like rheumatoid arthritis, systemic lupus crythematogus, and neurodegenerative diseases. The present sequence is a pre-proporative Mc1-1 are the treating faths to the present sequence.
Example 1; Page 23; 62pp; English
                         Detection of novel proteins involved in with proteins involved in apoptosis
                                                                   WPI; 1995-373811/48
                                                                                                                                                                                                                                 WO9528497-A1.
                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                    Mc1-1; Bax; apoptosis; cell death; regulation; Bc1-2; novel;
detection; ss.
                                                                                                                                                                                                                                                                                                                         Human Mcl-1 gene reverse PCR primer.
                                                                                                                                                                                                                                                                                                                                                      05-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1230 GAAAAGCAAGTGGCAAGAGGA 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel Mcl-l gene regulatory elements, useful for modulating expression of Mcl-l polypeptide or its variant which regulate apoptosis in neuronal or tumor cells -
                                                                                                                       (LJOL-) LA JOLLA CANCER RES FOUND
                                                                                                                                                  13-APR-1994;
                                                                                                                                                                           12-APR-1995;
                                                                                                                                                                                                      26-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                         AAT03166 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                            Sato
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                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 C; 2 G; 10 T; 0
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Pred. No.
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17;
                                        apoptosis
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                                        interaction
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AAZ39083/c
LD AAZ39083 standard; DNA; 20
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Best Local :
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                                                                                  The present invention describes antisense oligonucleotides which modulate the expression of novel anti-apoptotic bol-2-related proteins. The antisense oligonucleotides can be used as therapeutic agents to prevent or delay inflammation or tumour formation by promoting apoptosis in human cells or tissues. They can also be used as research agents to establish the function of particular genes and as diagnostic agents in sandwich assays for detecting the level of novel anti-apoptotic bol-2-related proteins in a sample. The antisense oligonucleotides given in the present invention were designed to target human Al and mol-1 anti-apoptotic bol-2-related protein nucleotide sequences. The present sequence represents an antisense oligonucleotide for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT03164-T031366 are primers used for the amplification of the human Mcl-1 gene. The Mcl-1 protein is a Bcl-2 related protein, the Mcl-1 protein was expressed and used to investigate the interactions of Mcl-1 with other proteins known to be involved in apoptosis (excluding the Bax protein). Proteins detected using this method can act as upstream activators or downstream effectors of a cellular protein such as Bax which induces apoptosis. If the protein is a Bcl-2 related protein apoptosis levels are decreased due to the protein binding to and inactivating Bax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1182 GGACTCCAAGCTGTAACTTC 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins are useful for inducing apo and treating associated diseases e.g. cancer - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Al; anti-apoptotic; bcl-2-related protein; antisense int
mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
inflammation; diagnosis; phosphorothloate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JAN-1999;
                                                                human mcl-l nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human mcl-1 anti-apoptotic bcl-2-related
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51;
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Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 other;

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      RESULT 10
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                                                                                                                                                                                                                                                                                     The present invention describes antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins. The antisense oligonucleotides can be used as therapeutic agents to prevent or delay inflammation or tumour formation by promoting apoptosis in human cells or tissues. They can also be used as research agents to establish the function of particular genes and as diagnostic agents in sandwich assays for detecting the level of novel anti-apoptotic bcl-2-related proteins in a sample. The antisense oligonucleotides given in the present invention were designed to target human Al and present sequence represents an antisense oligonucleotide sequence. The human mcl-1 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis and treating associated diseases e.g. cancer -
                                                                                                                                                                                                                                                     Sequence 20 BP; 0 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 31; Column 33; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Al; anti-apoptotic; bcl-2-related protein; antisense inhibition; mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour; inflammation; diagnosis; phosphorothioate; ss.
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llarity 100.0%;
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                                                                                                                                                                                      Score 20;
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Pred. No.
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                                                                                                                                                                      Mismatches
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5. 51;
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51;
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RESULT 11
AAZ39086/c
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Best Local S
Matches 20
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                         Human; Al; anti-apoptotic; bcl-2-related protein; antisense inhibition; mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
                                                                                          Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20420
                                                                                                                                                                                                                                                                                                                                                  2366 GGTGGATGGAGAGACATTTG 2385
                                                                                                                                        29-FEB-2000
                                                                                                                                                                                    AAZ39086;
                                                                                                                                                                                                                     AAZ39086 standard; DNA;
             inflammation; diagnosis; phosphorothicate;
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mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
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20; Conserv
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ilarity 100.0%;
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Pred. No.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis and treating associated diseases e.g. cancer - \frac{1}{2}
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                                                                                                                                                                                          Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
                                                                                                                                                                                                                                   Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20421
                                                                                                                                                                                                                                                                                                                   AAZ39087 standard; DNA;
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(ISIS-) ISIS PHARM INC
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                                                                                                                                                    synthetic.
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                                                                                                                                                                               inflammation;
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20; Conservative
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 The present invention describes antisense oligonucleotides which modulate
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mcl_1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
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                                                                                                         Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis and treating associated diseases e.g. cancer \dot{}
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ilarity 100.0%;
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diagnosis; phosphorothioate; ss.
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Pred. No.
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Column 33;

28pp; English

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             The present invention describes antisense oligonucleotides which modulate the expression of novel anti-apoptotic bol-2-related proteins. The antisense oligonucleotides can be used as therapeutic agents to prevent or delay inflammation or tumour formation by promoting apoptosis in human cells or tissues. They can also be used as research agents to establish the function of particular genes and as diagnostic agents in sandwich assays for detecting the level of novel anti-apoptotic bol-2-related proteins in a sample. The antisense oligonucleotides given in the present invention were designed to target human Al and mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The present sequence represents an antisense oligonucleotide for the
                                                                                                                                                                                                                                                                                                                                              Antisense oligonucleotides which modulate the expression of novel anti-apoptotic bol-2-related proteins are useful for inducing apopund treating associated diseases e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human cells or tissues. They can also be used as research agents to establish the function of particular genes and as diagnostic agents in sandwich assays for detecting the level of novel anti-apoptotic bcl-2-related proteins in a sample. The antisense oligonucleotides given in the present invention were designed to target human Al and mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The present sequence represents an antisense oligonucleotide for the
                                                                                                                                                                                                                                                                                                            Example 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 GGCGACTGGCAATGTTTGGC 69
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nucleotide sequence
                                                                                                                                                                                                                                                                                                            Column 33;
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Best Local
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                                                                                                                                                                                                                                                                              The present invention describes antisense oligonucleotides which modulate the expression of novel anti-apoptotic bcl-2-related proteins. The antisense oligonucleotides can be used as therapeutic agents to prevent or delay inflammation or tumour formation by promoting apoptosis in human cells or tissues. They can also be used as research agents to establish the function of particular genes and as diagnostic agents in sandwich assays for detecting the level of novel anti-apoptotic bcl-2-related proteins in a sample. The antisense oligonucleotides given in the present invention were designed to target human Al and manual antisense of the present invention were designed to target human Al and manual antisense of the present invention were designed to target human Al and manual antisense of the present invention were designed to target human Al and manual antisense of the present invention were designed to target human Al and manual antisense of the present invention were designed to target human Al and manual and manual antisense of the present invention were designed to target human Al and manual antisense of the present inventory between the present inventory between the present inventory between the present inventory by the pre
                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
mcl-l;
                                                                                                                                                                                                                                           present sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ackermann EJ,
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                                                                                                                   Local
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                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Al; anti-apoptotic; bcl-2-related protein; antis apoptosis; cancer; antiinflammatory; cytostatic;
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                                                                                                                Similarity
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51;
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 AI370619
7 BH635174
1 CO1095
AZ439313
BH855488
TA23F08P
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AI370619 ta40f05.x
BH635174 1008002H1
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AZ439313 1M0229J20
BH855488 SALK_0850
AL453160 T. brucei
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 source
        Tumor Gene Index
Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 431 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                 sequence.
AI370619
                                                                                                                                                                                                                                                                                    A1370619 43 bp mRNA linear EST 16-FEB-1 ta40f05.x1 Soares_total_fetus_ND5HF8_yw Homo saqbes_cDxA clone IMAGE:2046561 3' similar to SW:BPL1_HUMAN 0.16548 BCL2-RELATED PROTEIN A1 ;contains element TAR1 repetitive element ; mRNA
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Primates; Catarrhini; Hominid
1 (bases 1 to 43)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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7 AZ346753
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7 AZ323085
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7 AL761320948
AU009945
7 ABH849581
7 AH762626
7 BH849581
7 AH762626
7 BH792796
AA253295
7 AA2482001
7 AU7017
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AZ346753 1M0082E11
BHB63143 SALK, 0932
AU254252 AU254252
AU254252 AU254252
AZ331642 1M0059911
AZ469379 1M0282P14
AZ663912 1M0543J18
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AZ809484 2M0073F04
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Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                           Possible ligation site of ends cut
Reverse complemented post-ligation
Plate: 1008002 row: 36
                                                                                                                                                                                                                                                                                                                                                                             855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                              Stanford University
855 California Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Similarity
28; Conser
                                                                                                                                                                                                                                                                                                                                                               Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biological Sciences
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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; BescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, got to the web site www.zmdb.lastate.edu and follow the links for RescueMu.' Grid I was grown at Berkeley in 2001. DNA wa
                                                                                                                                                       /cultivar="mixed background W23/A188/B73"
/db xref="taxon:4577"
/clone_lib="1008 - RescueMu Grid I"
/tlssue_type="leaf"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="hH10B"
                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                           /organism="Zea mays"
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/db_xref="taxon:9606"
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                                                      42
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REFERENCE AUTHORS

SOURCE KEYWORDS VERSION ACCESSION DEFINITION Locus

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Matches Query Match

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16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/podymap'. The sequences of the clones represented by this GS sequences is also found there.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Gene Signature, 3'-directed cDNA sequence. We are not submitting the same cDNA sequence redundantly to DDBJ since 1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okubo,K.
BodyWap; human gene expression database
Unpublished (1995)
Contact: Okubo,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
                                                                                       Conservative
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                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxxon:966"
/clone_lib="Human adult (K.Okubo)"
/clone_lib="Human adult"
/dev_stage="adult"
/note="Organ: blood; Vector: l-gt-11; Site_1: Eco-RI;
Monocytes were prepared from blood by ficol1-hypaque,
percoll and T cell rosetting purification steps (purity:
96 %). mRNA was prepared from activated monocytes from a
patient with rheumatoid arthritis. mRNA was reverse
transcribed with MuLV. Using Eco-RI linkers CDNA was
cloned into l-gt-11 vector arms. The cDNA library was
screened by differential hybidization using radioactively
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                                                                                                                                                                                                                                          marked ss-cDNA from activated and non-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                       Score 15; DB 14;
Pred. No. 4.7e+03;
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1.3e+03;
                                                                                                                             Length 43;
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KEYWORDS
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                                                                                                       719 ACCTTCCAGAGTTA 732
                                                                                                                                                                         Local Similarity
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26 bp DNA linear GSS 03-OCT-200 IM0229J20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0229J20 R, DNA sequence.
A2439313
A2439313.1 GI:10563326
GSS.
house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
84112, USA
Tel: 801 585 5006
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CACACAGGAAACAGCTATGACCCclass: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
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1 (bases 1 to 26)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 26.
                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114/gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
                                                                                                                                                                                                                                                               12
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: PWD42nv; Purified genomic musculus C57BL/6J (male) was obtained fi Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="UUGC1M0229J20"
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                                                                                                                                                                      Score 14; DB 17; Pred. No. 1.4e+04
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                                                                                                                                                     Mismatches
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                                                                                                                                                                          ORGANISM
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BH855488
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 25)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, I., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 25)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis Genome Unpublished (2001)
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Direct Submission Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
                                      Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                          Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: TDNA tagged
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                                                                                                                                                                                                Trypanosoma brucei.
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                                                                                                                                                     łukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                 rypanosoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="ALK_085052.22.25.x"
/clone="ble="Arabidopsis thaliana TDNA insertion lines"
/clone="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.saik.edu/tdna_protocols.html"
a 1 c 5 g 13 t
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                           GI:11847458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bairell, Oxford University ......
Email: nelsayedetigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0032 row: B column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 bp DNA linear GSS 16-FEB-200
2M0032B19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0032B19 R, DNA sequence.
                                                                                                                        High quality sequence stop: 26.
Location/Qualifiers
                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                 University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Constructed at the Institute for Genomic Research (TIGR), ROCKVILLE, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucel (TREU927/4 GUTat 10.1) was mechanically sheat or give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small construction is the construction of the construction of the construction is described in detail in Smith, H. and Venter, J.C. (Making small construction).
                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B.
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                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/clone="UUGC2M0032B19"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                           /db_xref="taxon:10090"
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/strain="TREU927"
/db_xref="taxon:5691"
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Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                           Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0044 row: J column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                        University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B.
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LM0044J02F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0044J02 F, DNA sequence.
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1 (bases 1 to 29)
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                           USA
/clone="UUGC1M0044J02"
                        /db_xref="taxon:10090"
                                                 /organism="Mus musculus"
/strain="C57BL/6J"
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//lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
//lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No.
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"

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RESULT 9
AL761633
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AL761633
                                                                                                                Zuechtungsforschung, Carl von Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone MPF21. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the GERI-Kat project. GABI-Kat p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROSSO,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA
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Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                       Location/Qualifiers
/organism="Arabidopsis thaliana"
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Pred. No.
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Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZB09484 31 bp DNA linear GSS 20-FEB-200 2M0073F04R Mouse 10kb plasmid UUGClM library Mus musculus genomic clone UUGC2M0073F04 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                   Class: plasmid ends
High quality sequence stop: 31.
                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0073 row: F column: 04
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/db_xref="taxon:3702"
/db_xref="taxon:3702"
/db_xref="taxon:3702"
/clone="gk-227805-014266"
/clone=lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pACI61. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaian nuclear genome sequence were
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a 3 c
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                                                            musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0073F04"
                                          (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                          /clone_lib="Mouse 10kb plasmid UUGClM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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hydrodynamically sheared by repeated passage through a
D5 inch orifice at constant velocity. The sheared DNA
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3. 5.4e+04;
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EST 31-JUL-1998

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135 CGTCCTACAGATA 147
                                                                                                                                                                                                    Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.

CE 1 (bases I to 33)

Rs Naruse, K., Mitani, H. and Tanaka, M.

Medaka EST Project in University of Tokyo (2001)

AL Unpublished (2001)

Contact: Kiyoshi Naruse

Department of Biological Sciences

Graduate School of Science, University of Tokyo

Graduate School of Science, University of Tokyo

Graduate School of Science, University of Tokyo

Hongo 73-1, Bunkyo-Ku, Tokyo 113-0033, Japan
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                                                                                        TCAACAGCTTCAA
                                                                                                                                  TCAACAGCTTCAA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from UV irradiated OLHNI cell line cDNA
library (OLC) 5' end sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AU240558 UV irradiated OLHNI cell line cDNA library latipes cDNA clone OLc21.11d, mRNA sequence.
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                                                                                                                                                                                                                                                                                                         /organism="Oryzias latipes"
/Strain="HNI"
/db_xref="%taxon:8090"
/clone="0Lc21.11d"
/clone="DLc21.11d"
/clone=lib="UV irradiated OLHNI cell line cDNA library
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                      plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Lobases I to 36)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C. Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Ree, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauser and Wright, D., Weiss, R.
                                                                                                                                                                  Mouse whole genome scaffolding with paired
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba
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1 (bases 1 to 35)
Morimyo, M. and Mita, K.
Identification of expressed
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Schizosaccharomyces pombe
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35 bp mRNA linear EST 31-JI
AU009945 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc00705, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU009945.1 GI:3346625
308,
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    morimyo@nirs.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of Ml3mpl9 DNA and the direction of DN sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)" a 2 c 6 g 8 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4896"
/clone="spc00705"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h_minus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: M13mp19; The cDNA library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                     GI:10643091
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Pred. No. 5.7e+04;
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                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Length 35

DNA

Indels

0; Gaps

0;

linear GSS 04-OCT-200 ry Mus musculus genomic

GSS 04-OCT-2000

JOURNAL COMMENT REFERENCE AUTHORS TITLE

ACCESSION VERSION

DEFINITION

SOURCE

ORGANISM

KEYWORDS

RESULT 11 AU240558

Ъ QУ BASE COUNT ORIGIN

tags of Schizosaccharomyces

263-8555,

Query Match Matches

В 20

16

26

ORIGIN

Matches Query Match Best Local :

13;

end reads from 10kb

Murinae; Mus

Reilly

20 S. 2030 E., SLC,

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BASE COUNT

10

FEATURES

source

RESULT 12

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RESULT 14
BH849581
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Best Local
                                                                                                           JOURNAL
                                                                                                                                                         TITLE
                                                                                                                                                                                                                                     AUTHORS
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                       Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
                                                                                                                                                    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                 Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
BH849581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BH849581 36 bp DNA linear GSS 13-JUN-2002 SALK_069905.21.55.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_069905.21.55.x, DNA
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 10000 std E Plate: 0306 row: K column:
                                                                                                                               Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                               thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                вн849581
10010 N. Torrey Pines Road,
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801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114(gb)AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampiciliin resistance."
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Length: 10000 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA
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/clone="UUGClM0306K18"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, Tl-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mouse 10kb plasmid UUGC1M library"
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100.0%; Pr
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La Jolla, CA 92037, USA
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TITLE
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                                                                                                   TE 3 (bases 1 to 38)

RS Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.

Direct Submission

AL Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene Atig29750. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-KAt project. GABI-KAt is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

http://www.mpiz.koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana Eukaryota; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledoms; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence. AL762626
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13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA
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This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
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/db_ref="salk_069905.21.55.x"
/clone="salk_069905.21.55.x"
/clone="salk_069905.21.55.x"
/clone="salk_069905.21.55.x"
/clone="salk_069905.21.55.x"
/clone="salk_069905.21.55.x"
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/organism="Arabidopsis thaliana"
/strain="Columbia 0"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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. 5.7e+04;
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BASE COUNT
ORIGIN
Search completed: March 14, 2003, 08:29:33 
Job time: 738.181 secs
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/clone="GK-026F02-013759"
/clone="GK-026F02-013759"
/clone="Ib="Narabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC106. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant smilarity to the A. thalaha nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

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Title: Perfect score: Sequence:

US-09-869-894-18 3934 1 tccagtaaggagtc

Scoring table:

OLIGO\_NUC
Gapop 60.0 , Gapext

60

441362 seqs, 153338381 residues

Run

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OM nucleic

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nucleic search, using sw model

Copyright

GenCore version 5.1.4\_p5\_4578 (c) 1993 - 2003 Compugen Ltd.

Minimum Maximum

DB DB

seq

length:

Listing first 45 summaries

Word size

Tota1

number of hits satisfying

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parameters:

Database

Issued\_Patents\_NA:\*

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Result

Score

Match Length

DB

SUMMARIES

1188

US-08-607-269-1
PCT-US95-04600-1
US-08-607-269-3
US-09-226-568-29
US-09-226-568-29
US-09-226-568-29
US-09-226-568-29
US-09-226-568-29
US-09-226-568-29
US-09-226-568-29
US-09-226-568-29
US-09-226-568-39
US-09-22

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-08.607-269-1/c
; Sequence 1, Application US/08607269
; Patent No. 5702897
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                                       Query Match
Best Local S
Matches 21
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COMPUTER: TBM PC CONSYMS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURENT APPLICATION DATA:
APPLICATION UMBER: US/08/607,269
FILING DATE: 13-APR-1994
ATTORNEY/ACENT INFORMATION:
APPLICATION NUMBER: US 08/226,876
FILING DATE: 13-APR-1994
ATTORNEY/ACENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: 9-LJ 9882
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC com
1235 GCAAGTGGCAAGAGGATTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Interaction of Proteins Involved TITLE OF INVENTION: Cell Death Pathway NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Campbell
STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
                                                                                                            LENGTH: 21 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                         l Similarity
21; Conserv
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                                       0.5%; So clarity 100.0%; I Conservative 0;
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PCT-US92-09202-6
PCT-US93-07743-5
PCT-US93-07743-1
PCT-US93-07743-1
PCT-US93-07743-1
PCT-US92-09202-3
US-08-863-639A-73
                                                      Score 21;
Pred. No.
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PCT-US95-04600-1/c
PCT-US95-04600-1/c
Sequence 1, Application PC/TUS9504600
; GENERAL INFORMATION:
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PCT-US95-04600-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US95/CETLING DATE: 12-APR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Imbta, Richard J.
REGISTRATION NUMBER: 37,643
REGISTRATION NUMBER: 37,643
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: Interaction of Proteins Involved in a
TITLE OF INVENTION: Cell Death Pathway
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
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                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                       COUNTRY:
                                                                                                                                                             ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite
CITY: San Diego
                                                                                                          ZIP: 92122
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CITY: San Diego
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OTHER INFORMATION: Description of Artificial Sequence: antisense; OTHER INFORMATION: sequence US-09-226-568-19
                                                                                                              US-09-226-568-20/c
                                                                                                                                   RESULT 5
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ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ 98
TELECOMMUNICATION INFORMATION:
TELECHONE: (619) 535-9001
TELECHONE: (619) 535-9049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 19
                                   GENERAL INFORMATION:
APPLICANT: Ackerman
                                                                           Sequence 20, Application US/09226568 Patent No. 6001992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/09226568 Patent No. 6001992
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                  Query Match 0.5%; Score 20; DB 3; Best Local Similarity 100.0%; Pred. No. 9.8;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
APPLICANT: Bennett, C. Frank APPLICANT: Dean, Nicholas M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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APPLICATION NUMBER: US 08/226,876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                        20 GGCGACTGGCAATGTTTGGC 1
                                                                                                                                                                                                                           50 GGCGACTGGCAATGTTTGGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                   Ackermann, Elizabeth J.
                                                                                                                                                                                                                                                                   Conservative
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; OTHER INFORMATION:
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US-09-226-568-21
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US-09-226-568-22/C
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US-09-226-568-21/c
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; OTHER INFORMATION: sequence
US-09-226-568-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 21
                                                                                                                                                GENERAL INFORMATION:
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Patent No. 600199
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CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 20
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Best Local
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Best Local Similarity
                                                                                                                                                                 Sequence 22, Application US/09226568 Patent No. 6001992
                                                                                                                                                                                                                                                                                                                                                           Matches
              APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Micholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Antisense Modulation of No. 6001992eI Anti-apoptotic TITLE OF INVENTION: bcl-2-related Proteins FILE REFERENCE: ISPH-0337
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APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
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TITLE OF INVENTION: Antisense modulation of No. 6001992el Anti-apoptotic TITLE OF INVENTION: bc1-2-Related Proteins
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Local Similarity 100.0%;
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RESULT 8
US-09-226-568-23/c
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Best Local S
Matches 20
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic TITLE OF INVENTION: bc1-2-related Proteins FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 20
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                                                                                                                                                                                                                                                            Sequence 24, Application US/09226568 Patent No. 6001992
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SEQ ID NO 23
LENGTH: 20
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GENERAL INFORMATIC
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 22
LENGTH: 20
TYPE: DNA
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APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic TITLE OF INVENTION: bcl-2-Related Proteins
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APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ackermann, Elizabeth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: antisense OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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Similarity 100.0%;
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Pred. No.
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Pred. No.
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GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Bean, Micholas M.
APPLICANT: Marcusson, Eric G.

TITLE OF INVENTION: Antisense Modulation of No. 60
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT APPLICATION FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 20
TYPE: DNA
OPERANTSM: Artificial SCHOOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dean, Nicholas M.
APPLICANT: MATCUSSON, Eric G.
ATITLE OF INVENTION: Antisense Modulation of No. 600
TITLE OF INVENTION: bc1-2-Related Proteins
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT ETLING DATE: 199-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 20
TYPE: DNA
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US-09-226-568-26/c
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Best Local Similarity 100.
Matches 20; Conservative
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ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: antisense {\tt OTHER\ INFORMATION:} sequence
                                         FEATURE:
                                                     ORGANISM: Artificial Sequence
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Pred. No.
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US-09-226-568-27/c
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APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: Antisense modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: Active Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: Active Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION WINDER: US/09/226,568
CURRENT APPLICATION UNMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
TYPE: DNA
TYP
Query Match 0.5%; Score 20; DB 3
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches
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Best Local Similarity 100.0%;
Matches 20; Conservative (
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CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 20
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ackermann, Elizabeth J. APPLICANT: Bennett, C. Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dean, Nicholas M. APPLICANT: Marcusson, Eric G.
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                                                                                                                                                                  OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
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Local Similarity 100.0%;
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                                                                                                                                                                  Description of Artificial Sequence: antisense sequence
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Sequence 30, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Hoan, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: bcl-2-related Proteins
FILE REFERENCE: ISPH-0337
CURRENT EPILIAGTION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIAN Ver. 2.0
IENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-26-568-30
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APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
TITLE OF INVENTION: bcl-2-related Proteins
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
OTHER INFORMATION: sequence
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US-09-226-568-30/c
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US-09-226-568-29/c
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length: 50
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          GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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          10 US-09-884-814-4
10 US-09-263-959-900
10 US-09-263-959-904
10 US-09-263-959-904
10 US-09-828-034-31
10 US-09-828-034-31
19 US-10-194-594-12
19 US-10-194-594-12
10 US-09-811-824-5
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10 US-09-811-824-6
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3 12 US-10-143-108
6 9 US-10-026-914-10
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    Sequence 4, Appli
Sequence 900, App
Sequence 91, App
Sequence 11, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 59, Appli
Sequence 59, Appli
Sequence 59, Appli
Sequence 19, Appli
Sequence 22, Appli
Sequence 4, Appli
Sequence 10, Appli
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25	24	24	24	23	23	22	21	21	20	20	19	18	46	46	44	31	30	27	18	50	48	48	47	46	46
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US-09-755-088-1	US-10-180-762-27	US-09-804-717A-30	US-09-911-176B-27	US-09-735-995-73	US-09-735-995-17	us-09-263-959-1093	US-09-828-034-28	US-09-828-034-9	US-09-800-629A-27	US-09-863-806-85	US-09-736-863-16	US-09-961-077-1149	US-10-137-316-7	US-10-137-316-5	บร-09-007-093-16	US-09-912-263-155	US-09-976-736-27	US-09-873-676-74	US-09-969-373-2606	US-09-935-727-26	US-10-082-018-6	US-09-801-042-8	US-10-026-914-4	us-10-026-914-16	us-10-026-914-14
Sequence 1, Appli	Sequence 27, Appl	Sequence 30, Appl	Sequence 27, Appl	Sequence 73, Appl	Sequence 17, Appl	Sequence 1093, Ap	Sequence 28, Appl	Sequence 9, Appli	Sequence 27, Appl	Sequence 85, Appl	Sequence 16, Appl	Sequence 1149, Ap	Sequence 7, Appli	sequence 5, Appli	Sequence 16, Appl	Sequence 155, App	Sequence 27, Appl	Sequence 74, App1	Sequence 2606, Ap	•	Sequence 6, Appli	Sequence 8, Appli	Sequence 4, Appli	Sequence 16, Appl	Sequence 14, Appl

## ALIGNMENTS

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Sequence 900, Application US/09263959
PATENT NO. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
                                                                                                                                                                                                                                                                                                                                                                   : LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:U8R
US-09-884-814-4
                                                                                                                         RESULT 2
US-09-263-959-900
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US-09-884-814-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/124,293
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09884814 Patent No. US20020127600A1
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                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chen, Jin-Long
APPLICANT: Amaral, M. Catherine
APPLICANT: Amaral, M. Catherine
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2):
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 018781-01110US
CURRENT APPLICATION NUMBER: US/09/884,814
CURRENT APPLICATION NUMBER: US/09/884,814
CURRENT FILING DATE: 2001-06-18
  APPLICANT:
                                                                                                                                                                                                                                                453 GGAGCCTCTCGGGAAGC 469
                                                                                                                                                                                                       17 GGAGCCTCTCGGGAAGC 33
                                                                                                                                                                                                                                                                                       1 Similarity
17; Conserv
Rowen, Lee
Koop, Ben F.
                                                                                                                                                                                                                                                                                       ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                   0.4%;
                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                            Score 17; DB 10; Length 33; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                            Indels
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US-09-263-959-904
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-- rocal Similarity
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ZIP: 98104-70%
COMPOTER READABLE FORM:
COMPOTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPATIBLE FLOREM: PC COMPATIBLE
COM
            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERRNEZ/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 900
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ROWEN, LEE APPLICANT: ROWEN, LEE APPLICANT: KOOP, BER F. TITLE OF INVENTION. DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTINUMBER OF SEQUENCES: 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE_DOCKER NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Seed and Berry LLP STREET: 6300 Columbia Center, 701 Fifth Avenue
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RESULF 5
US-09-828-034-11
S-69uence 11, Application US/09828034
; Patent No. US20020064771A1
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US-09-263-959-921
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TELEFAX: (206) 682-6031
INFORMATION FOR SEG ID NO: 904:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                           Matches
                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 921, Application US/09263959 Patent No. US20020150891A1
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                                                                                                                                                                                               TELEFAX: (206) 682-603
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                           1148 ACCACCACCACCACCA 1163
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APPLICANT:
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                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
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                                                                                                                                     STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
STATE: Washing
                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                               NAME: McMasters, David D
REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 05-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
1 ACCACCACCACCACCA 16
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                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98104-7092
                                                                                                                                                                : 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
: US
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Koop, Ben F.
                                                            Conservative
                                                                                                                                         linear
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                                                                                                                                                     single
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100.0%; Pr
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                                                       Score 16; DB IV, __
; Pred. No. 6.5e+02;
...amatches 0;
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Pred. No.
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RESULT 7
US-09-828-034-31
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-30
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US-09-828-034-30
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                                                                                                                                                                                                                                                    Db
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PRIOR ETLING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNP US-09-828-034-11
              Sequence 31, Application US/09828034
Patent No. US20020064771A1
GENERAL INFORMATION:
APPLICANT: Zhong, Weidong
APPLICANT: Hong, Zhi
APPLICANT: Ferrari, Eric
TITLE OF INVENTION: HCV REPLICASE COMPLEXES
FILE REFERENCE: IN01165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30, Application US/09828034 Patent No. US20020064771A1 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 16; Conservative
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SEQ ID NO 11
LENGTH: 21
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APPLICANT: Zhong, Weidong
APPLICANT: Hong, Zhi
APPLICANT: Hong, Zhi
APPLICANT: Ferrari, Eric
TITLE OF INVENTION: HCV REPLICASE COMPLEXES
FILE REFERENCE: INO1165
CURRENT APPLICATION NUMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
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APPLICANT: Perrari, Eric
TITLE OF INVENTION: HCV REPLICASE COMPLEXES
FILE REFERENCE: INOL165
CURRENT APPLICATION NUMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
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PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 33
CURRENT APPLICATION NUMBER: US/09/828,034
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ORGANISM: Artificial Sequence
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; Pred. No. 6.6e+02;
0; Mismatches 0;
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RESULT 9
US-09-814-986-59
; Sequence 59, Application US/09814986
; Patent No. US20020068286A1
; GENERAL INFORMATION: Patrick W.
: APPLICANT: Kleyn, Patrick W.
                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature; LOCATION: (15)...(19); COTHER INFORMATION: Start sequence of the RNA polymerase L protein US-10-194-594-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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US-09-828-034-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-194-594-12/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: RECOMBINANT VSV FOR THE TREATMENT OF TITLE OF INVENTION: TUMOR CELLS
FILE REFERENCE: 52937200200
CURRENT APPLICATION NUMBER: US/10/194,594
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US 60/304,125
PRIOR FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/10194594 Publication No. US20030044386A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 21
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Best Local Similarity 100.0%;
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Best Local Similarity
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PRIOR APPLICATION NUMBER: U.S. 6
PRIOR FILING DATE: 2000-04-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_signal LOCATION: (2)...(12) OTHER INFORMATION: polyadenylation/transcription stop signal of the OTHER INFORMATION: glycoprotein (G) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Vesicular stomatitis virus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Artificial Sequence
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                  NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS:
                                                      TITLE OF INVENTION: COMPOSITIONS DIAGNOSIS OF
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ADDRESSEE: Pennie & Edmonds LLP
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Pred. No.
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Pred. No.
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                                                      FOR THE TREATMENT AND BODY WEIGHT DISORDERS,
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. 6.6e+02;
ches 0;
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1155 Avenue of the Americas

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CURRENT APPLICATION NUMBER: US/09/811,824
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,766
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 26
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Best Local Similarity 100.0%; Score 16; DB 9; L Matches 16; Conservative 0. Wirmar-1
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APPLICANT: Mattouss1, Hed1
APPLICANT: Mauro, J. Matthew
APPLICANT: Bawend1, Moung1 G.
APPLICANT: Sundar, Vikram C.
TITLE OF INVENTION: INORGANIC PARTICLE CONJUGATES
FILE REFERENCE: 01997-282001
                                                                                                  FEATURE: OTHER INFORMATION: Synthetically generated primer
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TELEX: 66141 PENN1E
INFORMATION FOR SEQ 1D NO: 59:
                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                        TYPE: DNA
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APPLICATION NUMBER: US/09/814,986
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
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FILING DATE: 24-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUTA A.
REGISTRATION UNUBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-100
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MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO:
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LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: New York
STATE: New York
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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; OTHER INFORMATION: Description Of Artificial Sequence: Caspase cDNA; OTHER INFORMATION: amplification primer US-09-045-620-3
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                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: primer US-09-728-466-19
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US-09-728-466-19/c
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SEQ ID NO 19
LENGTH: 30
TYPE: DNA
ORGANIEM: Artificial Sequence
                                                                        Query Match 0.4
Best Local Similarity 100.
Matches 16; Conservative
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SEQ ID NO 3
LENGTH: 30
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APPLICANT: He, Wanxia
TITLE OF INVENUTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/728,466
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BJORNSTI, MATY-Ann
APPLICANT: HALL, David
APPLICANT: KANG, Jason
TITLE OF INVENTION: MODULATORS OF EUKARYOTIC CASPASES
FILE REFERENCE: 209855,0027/27US
CURRENT APPLICATION NUMBER: US/09/045,620
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 5
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                       1148 ACCACCACCACCACCA 1163
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28 ACCACCACCACCA 13
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                                                                                             0.4%; Score 16; DB 10; 100.0%; Pred. No. 6.9e+02
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Pred. No. 6.9e+02;
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RESULT 13 US-09-954-697-50/c

Sequence 50, Application US/09954697

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APPLICANT: Alnemin; Emad S.
TITLE OF INVENTION: RECOMBIANT, ACTIVE CASPASES AND USSES
TITLE OF INVENTION: RECOMBIANT, ACTIVE CASPASES AND USSES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431D2
CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FAILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 50
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: PCR primer for small subunit of caspase-6
US-09-954-697-50
                                                                                                        COMPUTER READABLE ....

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-CDOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versio
REPLICATION NUMBER: US/09/817,513A
FILING DATE: 28-Jun-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: YOUNG J. Suh
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKST NUMBER: 27866/33886
TELLEOMMUNICATION INFORMATION:
TELLEPHONE: 312-474-6300
TELLEFAX: 312-474-6300
TELLEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
TOPOLOGY: Linear
TOPOLOGY: Linear
TOPOLOGY: Linear
                                                              TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-817-513A-22
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US-09-817-513A-22
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Query Match
Best Local Similarity
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TITLE OF INVENTION: Cytoplasmic modulators of Integrin Binding/Signaling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EE: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker, 6300 Sears Tower
0.4%;
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b; Pred. No. 6.9e+02;
Score 16;
Pred. No.
DB 9; Le
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                  Length 33;
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Вb
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Search completed: March 14, 2003, 10:59:24
Job time : 249.857 secs
                                                                                                                                                                                            ; OTHER INFORMATION: Synthetically generated primer US-09-811-824-4
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US-09-811-824-4
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                                                                                                                     Query Match
Best Local Similarity
Matches 16; Conserv
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,766
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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Publication No. US20020182632A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anderson, George P.
APPLICANT: Mattoussi, Hedi
APPLICANT: Mauro, J. Matthew
APPLICANT: Bawendi, Moungi G.
APPLICANT: Sundar, Vikram C.
TITLE OF INVENTION: INORGANIC PARTICLE CONJUGATES
FILE REFERENCE: 01997-282001
                                                                                                                                                                                                                           LENGTH: 34
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                 1148 ACCACCACCACCACCA 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1361 AGCTATGGAGGAGGAC 1376
                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AGCTATGGAGGAGGAC 24
                                                                ACCACCACCACCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                            0.4%;
illarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                25
                                                                                                                              0;
                                                                                                                                              Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                              DB 9;
7e+02;
                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                          Length 34;
                                                                                                                              Inde1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                            Gaps
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                                                                                                                            0
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Run

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Database :
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length:
            OLIGO_NUC Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-869-894-18
3934
1 tccagtaaggagtcggggtc.....aaatcttttattcaaataaa 3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        March 14, 2003, 04:35:16; Search time 5795.01 Seconds (without alignments) 17068.215 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24791104 seqs, 12571243825 residues
Cgn2_6/ptodata/1/pna/USO2_COMB.seq:*
('cgn2_6/ptodata/1/pna/USO3_COMB.seq:*
('cgn2_6/ptodata/1/p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pending_Patents_NA_Main:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12114646
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85:		82:	81:	80:	79.	70.	76:	75:	74:	73:	72:	71:	70:	69:	68:	67:	66:	65:	64:	63:	62:	61:	60:	59:	58:	57 :	56:	55:	54:	53:	52:	51:	50:	49:	48:	47:	46:	45:	44:	
/cgn2_6/ptodata/1/pna/US6041_COMB.seq:*	gn2_6/ptodata/1/pna/US6039_COMB.se	<pre>gn2_6/ptodata/1/pna/US6038_COMB.se</pre>	2_6/ptodata/1/pna/US6037_COMB.se	_6/ptodata/1/pna/US603	n2 6/ntodata/1/pna/US6034_COMB.Se	n2_6/ptodata/1/pna/US6033_COMB.se	2_6/ptodata/1/pna/US6032_COMB.s	2_6/ptodata/1/pna/US6031_COMB.s	n2_6/ptodata/1/pna/US6030_COMB.s	<pre>2_6/ptodata/1/pna/US6029_COMB.s</pre>	n2_6/ptodata/1/pna/US6028_COMB.s	<pre>2_6/ptodata/1/pna/US6027_COMB.s</pre>	2_6/ptodata/1/pna/US6026_COMB.s	2_6/ptodata/1/pna/US6025_COMB.s	2_6/ptodata/1/pna/US6024 COMB.seq	n2_6/ptodata/1/pna/US6023_COMB.seq	n2_6/ptodata/1/pna/US6022_COMB.s	2_6/ptodata/1/pna/US6021_COMB.s	<pre>2_6/ptodata/1/pna/US6020_COMB.s</pre>	<pre>2_6/ptodata/1/pna/US6019_COMB.s</pre>	n2_6/ptodata/1/pna/US6018_COMB.s	<pre>2_6/ptodata/1/pna/US6017_COMB.s</pre>	<pre>2_6/ptodata/1/pna/US6016_COMB.s</pre>	<pre>2_6/ptodata/1/pna/US6015_COMB.s</pre>	<pre>2_6/ptodata/1/pna/US6014_COMB.s</pre>	<pre>2_6/ptodata/1/pna/US6013_COMB.s</pre>	<pre>2_6/ptodata/1/pna/US6012_COMB.s</pre>	n2_6/ptodata/1/pna/US6011_COMB.s	2_6/ptodata/1/pna/US6010_COMB.s	2 6/ptodata/1/pna/US6009 COMB s	2 6/ptodata/1/pna/US6008 COMB.s	2_6/ptodata/1/pna/US6007_COMB.s	n2_6/ptodata/1/pna/US6006_COMB.se	gn2_6/ptodata/1/pna/US6005_COMB.se	n2_6/ptodata/1/pna/US6004_COMB.se	n2_6/ptodata/1/pna/US6003_COMB.se	gn2_6/ptodata/1/pna/US6002_COMB.seq	gn2_6/ptodata/1/pna/US6001_COMB.se	/cgn2_6/ptodata/1/pna/US6000_COMB.seq:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

c 21	c 20		c 18							c 11									c 2		Result No.
31	31	31	32	32	34	34	34	34	34	34	35	35	35	35	40	40	42	42	46	46	Score
0.8	0.8	0.8	0.8	0.8	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	1.0	1.0	1.1	1.1	1.2	1.2	Query Match Length
31	31	31	32	32	34	34	34	34	34	34	35	35	35	35	40	40	42	42	46	46	ength 1
œ	œ	8	10	œ	10	10	10	œ	8	œ	10	10	æ	œ	10	8	10	8	10	œ	DB
US-08-472-801-2255	US-08-472-801-2247	US-08-472-801-2231	US-08-668-235-2252	US-08-472-801-2252	US-08-668-235-2242	US-08-668-235-2239	US-08-668-235-2233	US-08-472-801-2242	US-08-472-801-2239	US-08-472-801-2233	US-08-668-235-2262	US-08-668-235-2258	US-08-472-801-2262	US-08-472-801-2258	US-08-668-235-2249	US-08-472-801-2249	US-08-668-235-2235	US-08-472-801-2235	US-08-668-235-2244	US-08-472-801-2244	ID
Sequence 2255, Ap	Sequence 2247, Ap	Sequence 2231, Ap	Sequence 2252, Ap	Sequence 2252, Ap	Sequence 2242, Ap	Sequence 2239, Ap	Sequence 2233, Ap	2242,	•	Sequence 2233, Ap	•	~			sequence 2249, Ap	Sequence 2249, Ap	ζ.	Sequence 2235, Ap	Sequence 2244, Ap	Sequence 2244, Ap	Description

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TITLE OF INVENTION: Method and Compositions for TITLE OF INVENTION: Reprogramming FILE REFERENCE: Hesed 2

CURRENT PELLOATION NUMBER: US/08/472,801

CURRENT FILING DATE: 1995-06-07

NUMBER OF 5ED ID NOS: 3601

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2244

LENGTH: 46

TYPE: DNA

ORGANISM: Homo sapiens
                              Sequence 244, Application US/08668235

GENERAL INFORMATION:

APPLICANT: Larry J. Smith

TITLE OF INVENTION: Methods and Compositions for Cellular

TITLE OF INVENTION: Reprogramming

FILE REFERENCE: Hesed-1

CURRENT APPLICATION NUMBER: US/08/668,235

CURRENT FILING DATE: 1996-06-17

EARLIER APPLICATION NUMBER: 07/748,997

EARLIER FILING DATE: 08/23/91

EARLIER FILING DATE: 08/23/91

EARLIER APPLICATION NUMBER: 08/426,781

EARLIER FILING DATE: 04/22/95

FEARLIER FILING DATE: 04/22/95
                                                                                                                                                                                                                                                                           RESULT 2
US-08-668-235-2244/c
                                                                                                                                                                                                                                                                                                                                                             Вþ
                                                                                                                                                                                                                                                                                                                                                                                                QΨ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-472-801-2244/c

: Sequence 2244, Application US/08472801

: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                     EARLIER
EARL1ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hesed 2
APPLICANT: Smith, Larry J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 GTCACTACCCTCGACGCCGCCGCCAGCAGGAGGAGGAGGAGGACGAG 579
                                                                                                                                                                                                                                                                                                                                                       46 GTCACTACCCTCGACGCCGCCGCCAGCAGGAGGAGGAGGAGGACGAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 1.2%; Score 46; DB 8; L
Local Similarity 100.0%; Pred. No. 8.6e-11;
res 46; Conservative 0; Mismatches 0;
APPLICATION NUMBER: 0: FILING DATE: 06/07/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0000000000000000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \begin{smallmatrix} 3 & 1 \\ 3 & 1 \\ 2 & 2 \\ 3 & 2 \\ 3 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 & 2 \\ 4 
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                   08/472,801
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0 US-08-668-235-2247

0 US-08-68-235-2255

PCT-US00-00969-19

8 US-09-483-184-19

US-08-472-801-2234

US-08-472-801-2254
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US-08-472-801-2240

US-08-472-801-2240

US-08-472-801-2240

US-08-472-801-2251

US-08-472-801-2251

US-08-472-801-2251

US-08-472-801-2253

US-08-668-235-2236

US-08-668-235-2248

0 US-08-668-235-2248

0 US-08-668-235-2250

US-08-668-235-2250

US-08-668-235-2253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for Cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Appl
Sequence 2134, Ap
Sequence 2234, Ap
Sequence 2240, Ap
Sequence 2240, Ap
Sequence 2250, Ap
Sequence 2251, Ap
Sequence 2259, Ap
Sequence 2236, Ap
Sequence 2238, Ap
Sequence 2238, Ap
Sequence 2231, Ap
Sequence 2251, Ap
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Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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ce 2247, Ap
ce 2255, Ap
ce 2255, Ap
19, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                          ; TYPE: DNA
; ORGAN1SM: HOMO
US-08-668-235-2235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-668-235-2235/c ; Sequence 2235, Application US/08668235 ; GENERAL INFORMATION:
                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/668,235
CURRENT FILING DATE: 1996-06-17
EARLIER APPLICATION NUMBER: 07/148,997
EARLIER FILING DATE: 08/23/91
EARLIER APPLICATION NUMBER: 08/426,781
EARLIER FILING DATE: 04/22/95
EARLIER FILING DATE: 04/22/95
EARLIER FILING DATE: 04/22/95
EARLIER FILING DATE: 04/22/95
EARLIER FILING DATE: 04/07/95
EARLIER FILING DATE: 03/07/95
EARLIER FILING DATE: 03/07/95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-08-472-801-2235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-472-801-2235/c ; Sequence 2235, Application US/08472801 ; GENERAL INFORMATION:
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                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2235
LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/472,801
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 3601
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 2235
LENGTH: 42
          Best Local Similarity 100.0%;
Matches 42; Conservative (
                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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Best Local Similarity 100.0%;
Matches 46; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2244
LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hesed 2
APPLICANT: Smith, Larry J.
TITLE OF INVENTION: Method and Compositions
TITLE OF INVENTION: Reprogramming
FILE REFERENCE: Hesed 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 3629 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                              sapiens
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100.0%;
                              1.1%; Score 42;
100.0%; Pred. No.
               0;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46;
Pred. No.
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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APPLICANT: Larry J. Smith
TITLE OF INVENTION: Methods and Compositions for Cellular
TITLE OF INVENTION: Reprogramming
FILE REFERENCE: Hesed-1
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               DB 10;
8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8;
8e-09;
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8.6e-11;
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                           Length 42;
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 Indels
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US-08-668-235-2249/c

Sequence 2249, Application US/08668235

GENERAL INFORMATION:
APPLICANT: Larry J. Smith

TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: Reprogramming
FILE REFERENCE: Hesed-1

CURRENT APPLICATION NUMBER: US/08/668,235

CURRENT FILING DATE: 1996-06-17

EARLIER APPLICATION NUMBER: 07/748,997

EARLIER FILING DATE: 08/23/91
RESULT 7
US-08-472-801-2258/c
Sequence 2258, Application US/08472801
GENERAL INFORMATION:
APPLICANT: Hesed 2
APPLICANT: Smith, Larry J.
TITLE OF INVENTION: Method and Compositions for Cellular
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                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens US-08-668-235-2249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 08/426,781
EARLIER FILING DATE: 04/22/95
EARLIER APPLICATION NUMBER: 08/472,801
EARLIER FILING DATE: 06/07/95
RUMBER OF SEQ ID NOS: 3629
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2249
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APPLICANT: Smith, Larry J.
APPLICANT: Smith, Larry J.
TITLE OF INVENTION: Method and Compositions for Cellular
TITLE OF INVENTION: Reprogramming
FILE REFERENCE: Hesed 2
CURRENT APPLICATION NUMBER: US/08/472,801
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 3601
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2249
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                                                                                                                                                                                                                                                                                                                      Ouery Match 1.0%; Score 40; DB 10; Length 40; Best Local Similarity 100.0%; Pred. No. 7.7e-08; Matches 40; Conservative 0; Mismatches 0; Indels
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Best Local (
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100.0%; Pred. No. 7.7e-08;
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CURRENT APPLICATION NUMBER: US/08/472,801
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 3601
SOETWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2258
LENGTH: 35
TYPE: DNA
ORGANISM: Homo sapiens
US-08-472-801-2258
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US-08-472-801-2262/c
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                                                                                                                          CURRENT ADPLICATION NUMBER: US/08/668, 235
CURRENT FILING DATE: 1996-06-17
EARLIER APPLICATION NUMBER: 07/748, 997
EARLIER FILING DATE: 08/23/91
EARLIER FILING DATE: 08/23/91
EARLIER FILING DATE: 04/22/95
EARLIER FILING DATE: 04/22/95
EARLIER FILING DATE: 06/07/95
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; ORGANISM: Homo sapiens US-08-668-235-2258
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Best Local S
Matches 35
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CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 3601
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2262
LENGTH: 35
TYPE: DNA
TYPE: DNA
                                                   NUMBER OF SEQ ID NOS: 3629
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2258
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                              Sequence 2258, Application US/08668235 GENERAL INFORMATION:
APPLICANT: Larry J. Smith
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Best Local Similarity 100.0%;
Matches 35; Conservative (
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APPLICANT: Smith, Larry J.
APPLICANT: Smith, Larry J.
TITLE OF INVENTION: Method and Compositions for Cellular
TITLE OF INVENTION: Reprogramming
FILE REFERENCE: Hesed 2
FILE REFERENCE: Hesed 2
                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Methods and Compositions for Cellular TITLE OF INVENTION: Reprogramming FILE REFERENCE: Hesed-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: Hesed
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                                      TYPE: DNA
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; Pred. No. 2.2e-
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В

Length 34;

Inde1s

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Gaps

0;

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TITLE OF INVENTION: Methods and Compositions for Cellular TITLE OF INVENTION: Reprogramming FILE REFERENCE: Hesed-1 CURRENT APPLICATION UNMER: US/08/668,235 CURRENT FILING DATE: 1996-06-17 EARLIER APPLICATION NUMBER: 07/748,997 EARLIER APPLICATION NUMBER: 08/426,781 EARLIER FILING DATE: 08/23/91 EARLIER FILING DATE: 08/23/95 EARLIER APPLICATION NUMBER: 08/472,801 EARLIER APPLICATION NUMBER: 08/472,801 EARLIER APPLICATION NUMBER: 08/472,801 EARLIER APPLICATION NUMBER: 08/472,801 EARLIER FILING DATE: 06/07/95 NUMBER OF SEQ ID NOS: 3629 SOPTWARE: FASTSEQ for Windows Version 3.0 SEG ID NO 2262 FORDS NUMBER: SANTAMERE OF SEG ID NOS: 3629 SEG ID NO 2262 FORDS NUMBER: SANTAMERE FASTSEQ FOR WINDOWS VERSION 3.0 ERNGTH: 35
          RESULT 12
US-08-472-801-2239/c
; Sequence 2239, App
                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-08-472-80I-2233
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; ORGANISM: Homo sapiens
US-08-668-235-2262
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US-08-668-235-2262/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2233, Application US/08472801
GENERAL INFORMATION:
APPLICANT: Hesed 2
CURRENT APPLICATION NUMBER: US/08/472,801
CURRENT ETILS OF DATE: 1995-06-07

NUMBER OF TAXABLE OF THE STATE OF TAXABLE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF TAXABLE OF THE STATE OF THE STATE OF TAXABLE OF THE STATE OF TAXABLE OF TAXABL
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2233
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                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                      Query Match
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Best Local (
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 34
TYPE: DNA
                                                                                                                                                             150 CCCGGGAGGGCGACTTTTGGCTACGGAGAAGGAG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            628 GCCACCGGCGCCAAGGACACAAAGCCAATGGGCAG 662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 GCCACCGGCGCCAAGGACACAAAGCCAATGGGCAG 1
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Similarity 100.0%;
35; Conservative
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          Application US/08472801
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                                                                                                                                                                                                                                                                                                                    0.9%; Score 34; DB 8; 100.0%; Pred. No. 6.9e-0
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Pred. No.
                                                                                                                                                                                                                                                                                            Mismatches
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3. 2.2e-05;
ches 0;
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                                                                                  CURRENT APPLICATION NUMBER: US/08/668,235
CURRENT FILING DATE: 1996-06-17
EARLIER APPLICATION NUMBER: 07/748,997
EARLIER FILING DATE: 08/23/91
EARLIER APPLICATION NUMBER: 08/426,781
EARLIER FILING DATE: 04/22/95
EARLIER FILING DATE: 08/472,801
EARLIER FILING DATE: 06/07/95
NUMBER: 05/07/95
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NUMBER: 05/07/95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-472-801-2242/c; Sequence 2242, Application US/08472801
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 2233, Application US/08668235 GENERAL INFORMATION:
APPLICANT: Larry J. Smith
TITLE OF INVENTION: Methods and Compos
TITLE OF INVENTION: Reprogramming
FILE REFERENCE: Hesed-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/472,801
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 3601
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2242
LENGTH: 34
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2233 LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hesed 2
APPLICANT: Smith, Larry J.
TITLE OF INVENTION: Method and Compositions for Cellular
TITLE OF INVENTION: Reprogramming
FILE REFERENCE: Hesed 2
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Best Local Similarity 100.0%;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2239
LENGTH: 34
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Best Local Similarity 100.0%; F
Matches 34; Conservative 0;
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APPLICANT: Smith, Larry J.
APPLICANT: Smith, Larry J.
TITLE OF INVENTION: Method and Compositions
TITLE OF INVENTION: Reprogramming
FILE REFERENCE: Hesed 2
CURRENT APPLICATION NUMBER: US/08/472,801
CURRENT FILING DATE: 1995-06-07
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Pred. No. 6.9e-
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Mismatches 0;
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Length 34;

Indels

0;

Gaps

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В QУ

В QΥ

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RESULT 15

US-08-668-235-2239/c
US-08-668-235-2239/c
Sequence 2239, Application US/08668235
Sequence 2239, Application US/08668235
GENERAL INFORMATION:
APPLICANT: Larry J. Smith
APPLICANT: Larry J. Smith
ITITLE OF INVERTION: Methods and Compositions for Cellular
ITITLE OF INVERTION: MUMBER: US/08/668,235
CURRENT FILING DATE: 1996-06-17
EARLIER FILING DATE: 08/23/91
EARLIER FILING DATE: 08/23/91
EARLIER FILING DATE: 04/22/95
EARLIER FILING DATE: 04/22/95
EARLIER FILING DATE: 06/07/95
NUMBER OF SEQ ID NOS: 3629
SEQ ID NO 2334
TYPE: DNA
ORGANISM: Homo sapiens
US-08-668-235-2239
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Search completed: March 14, 2003, 10:28:01 Job time: 5797.01 secs
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                                                                                                                                                                                Query Match 0.9%; Score 34; DB 10; Length 34; Best Local Similarity 100.0%; Pred. No. 6.9e-05; Matches 34; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 34; Conservative 0; Mismatches 0;
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                                                                                          Length 34;
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Total number of hits satisfying chosen parameters:
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Perfect score:
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3934
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              /cgn2_6/ptodata/2/pna/PcT_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
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'cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

24	c 22	c c 20			17	c 16	c 15	c 14	13	c 12	11	c 10	0	8	0 /			4	-	c 2		No.	Result
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8	8	7	9	9	9	9	9	8	8	8	8	8	8	8	8	8	8	8	9	9	
US-10-050-902-298	US-10-050-902-297	US-10-287-787-13609	US-60-427-836-321372	US-60-427-836-65488	US-60-427-808-409599	US-60-427-808-179014	US-60-427-808-136571	US-10-355-577-870929	US-10-355-577-476248	US-10-355-577-106353	US-10-355-577-7439	US-10-310-188-62082	US-10-310-188-29017	US-10-310-188-48654	US-10-310-188-79759	US-10-236-392-255	US-10-310-188-31362	US-10-303-778-16089	US-60-449-155-609	US-60-427-836-571386	
298,	Sequence 297, App	Sequence 13609, A	Sequence 321372,	Sequence 65488, A	Sequence 409599,	Sequence 179014,	Sequence 136571,	Sequence 870929,			Sequence 7439, Ap	Sequence 62082, A	Sequence 29017, A	Sequence 48654, A	Sequence 79759, A	Sequence 255, App	Sequence 31362, A	Sequence 16089, A	Sequence 609, App	Sequence 571386,	

## RESULT 1 US-10-236-392-256/c GENERAL INFORMATION: Sequence 256, Application US/10236392

ALIGNMENTS

APPLICANT: Anderson, I APPLICANT: Boldog, Fe APPLICANT: Burgess, C APPLICANT: Casman, St APPLICANT:
APPLICANT:
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APPLICANT: APPLICANT: Gorman, Linda Grosse, William M Gusev, Vladamir Miller, Charles | Millet, Isabelle MacDougall, John R Malyankar, Uriel M Ellerman, Karen Gerlach, Valerie LaRochelle, William Kekuda, Edinger, Shlomit, Crabtree, Chapoval, Andrei Catterton, Elina Boldog, Ferenc L Ramesh Stacie J Catherine, David W Julie H

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: APPLICANT:
APPLICANT: APPLICANT:
APPLICANT:
APPLICANT: Peyman, John A Rastelli, Luca Reiger, Daniel K Rothenberg, Mark E Padigaru, Muralidhara Patturajan, Meera Pena, Carol A Shenoy, Suresh

APPLICANT: SHEWLY, SHEWLY, APPLICANT: SHEWLY, FILING DATE: 2001-09-1

SAME

PRIOR APPLICATION NUMBER: US60/357,303

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RESULT 2
US-10-293-338-8053/c
US-10-293-338-8053/c
(Sequence 8053, Application US/10293338
; GENERAL INFORMATION:
GENERAL INFORMATION: LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
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; OTHER INFORMATION: Description of Artificial Sequence: probe US-10-236-392-256
                                                                                                                                                                                                                        RESULT 3
US-10-310-188-79749/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; Homo sapiens US-10-293-338-8053
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PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: US99/659,634
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: US60/318,120
PRIOR APPLICATION NUMBER: US60/318,130
PRIOR APPLICATION NUMBER: US60/318,130
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
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        CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 79749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 794
SOFTWARE: Custom
SEQ ID NO 256
LENGTH: 25
                                                                                                                                                                Sequence 79749, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGemonics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 8053
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Best Local :
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CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
                                                                                                       TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF TITLE OF INVENTION: USES THEREOF FILE REFERENCE: 47487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US60/367,753
PRIOR FILING DATE: 2002-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 24
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ENGTH: 24
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Pred. No.
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. 0.26;
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0.079;
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RESULT 4
US-60-420-836-454577
US-60-420-836-454577, Application US/60427836
Sequence 454577, Application US/60427836
GENERAL INFORMATION:
APPLICANT: Xuee Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
TITLE OF INVENTION: MUMBER: US/60/427,836
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Best Local Similarity
Watches 24; Conserva
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RESULT 6
US-10-110-188-7862/c
US-10-310-188-7862/c
; Sequence 7862, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: ROSettaGemonics
; APPLICANT: ROSettaGemonics
; TITLE OF INVENTION: USES THEREOF
; FITLE OF INVENTION: USES THEREOF
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US-10-310-188-2068/c
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NUMBER OF SEQ ID NOS: 699466
SOFTWARE: MICOCORTRAY Probe Sequence Listing SEQ ID NO 444577
LENGTH: 25
TYPE: DNA
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Best Local S
Matches 23
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GENERAL INFORMATION:
APPLICANT: ROSettaGemonics
TITLE OF INVENTION: BIGINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
FILE REFERENCE: 47487
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2068
LENGTH: 22
TYPE: DNA
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Best Local Similarity
Matches 22; Conservat
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Local Similarity 100.0%; Pred. No.
les 23; Conservative 0; Mismatc
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100.0%; Pred. No.
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. 0.84;
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US-10-310-188-73447/c
Sequence 73447, Application US/10310188
GEBERAL INFORMATION:
APPLICANT: ROSettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SEQ ID NO 73447
INVENTION 1214
SEQ ID NO 73447
                                                                                                                                                                                                                                                                                                       US-10-355-577-900097
Sequence 900097, Application US/10355577
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of
FILE REFERENCE: 3121
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; ORGANISM: Homo sapiens
US-10-310-188-7862
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RESULT 9
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; ORGANISM: Homo sapien
US-10-355-577-900097
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Matches
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Best Local S
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CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 900097
LENGTH: 25
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CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 7862
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Best Local Similarity
Matches 21; Conserv
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100.0%; Pr
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FILE REFERENCE: 47487

CURRENT APPLICATION NUMBER: US/10/310,188

CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.1

SEQ ID NO 81944

LENGTH: 20

TYPE: DNA

ORGANISM: Homo Sapiens

US-10-310-188-81944
                                                                                                     Sequence 57, Application US/10169983
GENERAL INFORMATION:
APPLICATIVE TAKARA Shuzo Co., Ltd.
TITLE OF INVENTION: Therapeutic agents
FILE REFERENCE: 01-011-PCT
CURRENT APPLICATION NUMBER: US/10/169,983
CURRENT FILING DATE: 2002-07-14
PRIOR APPLICATION NUMBER: UJ 2000-4989
PRIOR APPLICATION NUMBER: UJ 2000-4989
PRIOR APPLICATION NUMBER: UJ 2000-303711
PRIOR APPLICATION NUMBER: UJ 2000-303711
PRIOR FILING DATE: 2000-10-33
NUMBER OF SEQ ID NOS: 61
SEQ ID NO 57
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US-10-169-983-57
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CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SOFTWARE: Patentin version 3.1
SEQ ID NO 3254
LENGTH: 20
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GENERAL INFORMATION:
APPLICANT: ROSettaGenomics LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 45282
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Best Local
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Best Local Similarity
Matches 20; Conserv
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY (
TITLE OF INVENTION: USES THEREOF
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ORGANISM: Homo sapiens
                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Designed primer based on nucleotide sequence of
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                                                                                         ENGTH: 20
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Pred. No.
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: OTHER INFORMATION: human myeloid leukemia cell differentiation US-10-169-983-57

protein-1

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RESULT 12
US-10-169-983-58/c
; Sequence 58, Application US/10169983
; Sequence 58, Application US/10169983
; GENERAL INFORMATION:
APPLICANT: Thexara Shuzo Co., Ltd.
TITLE OF INVENTION: Therapeutic agents
FILE REFERENCE: 01-011-07
; CURRENT APPLICATION NUMBER: US/10/169,983
; CURRENT FILING DATE: 2002-07-14
; PRIOR APPLICATION NUMBER: J7 2000-4989
pRIOR APPLICATION NUMBER: J7 2000-4989
pRIOR APPLICATION NUMBER: J7 2000-303711
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEO ID NOS: 61
                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of
FILE REFERENCE: 3528
CURRENT APPLICATION NUMBER: US/60/427,808
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEO ID NOS: 982914
SEO ID NO 23817
LENGTH: 25
RESULT 14
US-10-293-338-1275/c
; Sequence 1275, Application US/10293338
                                                                              В
                                                                                                                                                                                                ; TYPE: DNA ; ORGANISM: Mus musculus US-60-427-808-23817
                                                                                                                                                                                                                                                                                                                                                                                                         US-60-427-808-23817; A: Sequence 23817; A:
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FEATURE:
OTHER INFORMATION: Designed primer based on nucleotide sequence of OTHER INFORMATION: human myeloid leukemia cell differentiation pro-US-10-169-983-58
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LENGTH: 20
TYPE: DNA
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Best Local :
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Best Local :
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APPLICANT: RosettaGenomics LTD
TITLE OF INVENTION: BIOLNFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 45282
CURRENT APPLICATION NUMBER: US/10/293,338
CURRENT FILLING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SOFTWARE: Patentin version 3.1
SEQ ID NO 1275
LENGTH: 19
TYPE: DNA
ORGANISM: Homo saplens
US-10-293-338-1275
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-10-310-188-57069/c
Sequence 57069, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROSettaGemonics
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                                                                                                                                                                                                ; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-57069
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Search completed: March 14, 2003, 10:49:54
Job time: 1078.55 secs
                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: U5/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57069
LENGTH: 19
                                                                                                                                                  Query Match 0.5%;
Best Local Similarity 100.0%;
                                                                                                                                   Matches
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TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
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Best Local :
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                                                                                                 1133 GTTGACTTTTAACCAACCA 1151
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                                                                   GTTGACTTTTAACCAACCA
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Pred. No.
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 50
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3934
1 tccagtaaggagtc
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em_estmu:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 6	c 5	c 4	c 3	c 2	1	Result
18	18	19	21	23	30	Score
0.5	0.5	0.5	0.5	0.6	0.8	Query Match I
44 1	35 1	49 9	34 1	26 1	31 9	Query Match Length DB
7 AZ453451	7 AZ304663	AI569150	7 AZ343185	7 AZ365602	9 AA463890	Query Score Match Length DB ID
AZ453451 1M0254P10	AZ304663 1M0004016	AI569150 tr83a03.x	AZ343185 1M0076C22	AZ365602 1M0112017		Description

45	44	43	42	41	40	c 39					c 34		32	31	30	c 29	28			c 25			c 22		20		c 18									c 9		
15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	17	17	17
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AU1068	AU1068	AU1035	AU102484	.9 EP(2)	zq85c0	26 1M0151I1	.4 2M0034A2	)3 SALK_094	0 1M0155P1	4 2M0287M0	AZ936680 2M0193D01	9 r436 non	ŭ	1 1M0300G0	19 HNC		65781	89134	9399	0222	632020 1M0486P2	2 1M0541A0	1 T. bruce	5 1M0081C0	AZ829628 2M0107I05	5 1M0167P0	3 2M0094I2	47343 2M0210G0	512393 1M035	405428 IM0:	449706 1MO	860972	784648 2M00	622226 1M0455A2	Z315293 1M0032P2	Z637149 1M049	8644 y152h05.r	AZ403083 1M0170P09

## ALIGNMENTS

TITLE JOURNAL COMMENT REFERENCE AUTHORS ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM RESULT 1 AA463890 LOCUS DEFINITION Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 31)
1 (bases 1 to 31)
1 (bases 1, Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Rylie, T., Waterston, R. and Wilson, R.
Washly, Merck EST Project 1997
Unpublished (1997)
Unpublished (1997)
Contact: Wilson RK Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand AAA63890 3.51 Soares\_NhhmPu\_S1 Homo sapiens cDNA clone IMAGE:812645 3. similar to SW:WCL1\_HUMAN Q07820 INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL1.; mRNA sequence. AA463890 AA463890.1 GI:2188774 human

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JOURNAL
COMMENT
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KEYWORDS
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AUTHORS
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AZ365602/c
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Rukaryota; Metazoa; Chordata; Craniata; verturalidae; Murinae; .....
Rukaryota; Metazoa; Chordata; Craniata; verturalidae; Murinae; .....
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; .....
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; .....
(Dases 1 to 26)
1 (Dases 1 to 26)
1 (Dases 1 to 26)
1 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Pedersen,T., Reilly
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M. Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0112 row: 0 column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                      University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                    Contact: Robert B.
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AZ365602.1 GI:10479302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1M0112017F Mouse 10kb plasmid UUGCLM library Mus musculus clone UUGCLM0112017 F, DNA sequence.
                                                                                               High quality sequence stop: 26.
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Location/Qualifiers
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                                                                                                                                                                                                                                                           USA
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/strain="C57BL/6J"
/db_xref="taxon:10090"
                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:812645"
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/db_xref="GDB:6043555"
                                                                           Location/Qualifiers
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/tissue_type="P_ooled human melanocyte, fetal heart, and
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Pred. No.
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1148 ACCACCACCACCACCAAAACCAG 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A2343185 34 bp DNA linear GSS 29-SEP-20: IM0076C22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0076C22 R, DNA sequence.
                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 22
Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ343185.1 GI:10421362
                                                                                                                                                                                                                                                                                                                                     308,
                                                                                 quality sequence stop: 34.
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                                                                                                             plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="UUGCIM0112017"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"_
/organism="Mus musculus"
                                                  Location/Qualifiers
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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. 9.9;
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                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Life Technologies catalog #. 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
AI569150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -40UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI569150.1 GI:4532524
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                                 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013" 7 c 2 g 22 t
                                                                                                                                                                /clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2224876"
                                                                                                                                                                                                                                                                                                                                                         r: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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sapiens cDNA clone IMAGE:2224876 3',
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AUTHORS
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Best Local Similarity 100.0%; Pred. No.
Matches 19; Conservative 0; Mismatcl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0004 row: O column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 35)

Parhor M. Beacorn.T., Duval, B., Hamil, C.,
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University of Utah
Rm. 308, Biomedical
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Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
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(http://www.law.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114 gbl hF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplcillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="QUGCIM0004016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Mouse 10kb plasmid UUGClM library"
/sex="Male"
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b. 9.5e+02;
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REFERENCE AUTHORS

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AVA DNA linear GSS 04-OCT-200
1M0254P10R Mouse lokb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0254 row: P column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
1 (bases 1 to 44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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801 585 7177
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http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114(gb)AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli x110-Gold (Stratagene) cells and selected for ampiciliin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C5/BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
/c1one="UUGC1M0254P10"
                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Std Error: 0.00
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3.1e+03;
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AUTHORS
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               BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 bp DNA linear GSS 03-0CT-200 IM0170P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0170P09 R, DNA sequence.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rei
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 010 row: p column: 09
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
Unpublished (2000)
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Mammalia; Eutheria;
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nouse mouse
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ilarity 100.0%;
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                            adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gil4732114/gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                   musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0170P09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone__lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="c57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 17; L; Pred. No. 3.le+03;
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on Niederhausern,A.
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VERSION
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JOURNAL
         Best Local Similarity
                          Query Match
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Size: 953
High quality sequence stops: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 953
Std Error: 0.00
Seq primer: Ml3Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , M., Hiltman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohifing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. The Washu-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarriini; Hominidae; Homo.

1 (bases 1 to 40)

1 (bases 1 to 40)

1 (bases 1 to 40)

1 (bases 1 to 40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.4%; Score 17; DB 17; Length 28; ilarity 100.0%; Pred. No. 1e+04; Conservative 0; Mismatches 0; Indels
                                                                    /db_xref="taxon:9606"
/clone="IMAGE:161913"
                                                                                                                                                                                                                                                                                                      /sex="Female"
                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares breast 3NbHBst"
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                        ity sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GDB:57611
         0.4%;
     Score 17;
Pred. No.
       DB 14; Length 40; 9.9e+03;
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AUTHORS
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VERSION
KEYWORDS
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AZ637149/c
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Query Match
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High quality sequence stop: 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0496 row: F column: 19
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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University of Utah
Min. 308, Biomedical Polymers Res
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Unpublished (2000)
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 43)
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43 bp DNA linear GSS 13-DEC-200
1M0496F19F Mouse 10kb plasmid UUGClM library Mus musculus genomic
clone UUGClM0496F19 F, DNA sequence.
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                                                                                                Laboratory Mouse DNA Resources (Continued Line)
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi1472114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC1M0496F19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus'
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/lab_nomic_DNA from M.
   0.4%;
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Score 17;
Pred. No.
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   DB 17;
. 9.8e+03;
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RESULT 10
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1M0032P20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0032P20 F, DNA sequence.
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Insert Length: 10000 Std Error:
Plate: 0032 row: p column: 20
Seq primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
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house mouse.
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AZ315293.1 GI:10362003
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Location/Qualifiers
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Contact: Robert B. Weiss
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gi4 1732114 [gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and constituted the charact adaptors on the shared adaptors of the shared adaptors on the shared adaptors of the 
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                                                                                                            purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Col1 strain xL10-Gold, T1-resistant, F-"
/note="Yector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC1M0032P20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mouse 10kb plasmid UUGClM library"
   0.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
   Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Std Error: 0.00
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      DB 17; Length 19; 3.4e+04;
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      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (baseS 1 to 20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ622226.1 GI:11744416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
      0.4%;
100.0%;
      Score 16; pred. No.
            DB 17; Length 20; 3.4e+04;
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Matches
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Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0455 row: A column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and slze-selected for a 9.5 to
purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                            10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gli4732114/gb)AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0455A24"
/clone_lib="Mouse 10kb plasmid UUGClM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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              Query Match
Best Local Similarity
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Mand Wright,D.,Weiss,R., Mand Wright,D.,Weiss,R., Stokes, Weisselberger, Weis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: |
Plate: 0027 row: P column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 23.
Location/Qualifiers
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                         10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil473211/gb)haf129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll xL10-Gold (Stratagene) cells and selected for ampicallin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end: eat constant velocity. The sheared DNA polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/clone="UUGC2M0027P11"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
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                 0.4%;
              Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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Query Match
Best Local Similarity
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Welss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emmail: ddunnégenetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0167 row: A column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
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Contact: Robert B.
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23 bp DNA linear GSS 2: 2M0167A16F Mouse 10kb plasmid UUGClM library Mus musculus clone UUGC2M0167A16 F, DNA sequence.
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Fax: 801 585 7177
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                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orlifee at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gii4732114 | gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone="UUGC2M0167A16"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0248 row: M column: 02
Seq primer: CGTTGTAAAAACGACGGCCAGT
Class: plasmid ends
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Utah Genome Center University of Utah
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Contact: Robert B. Weiss
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AZ449706.1 GI:10603768
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Fax: 801 585 7177
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                                                                                                                                                                                                               10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMPA2 (gil4733114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                         chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.  
   15 c   1 g   1 t
                                                                                                                                                                                                                                                                                                                                                                                                                                      was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
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      0.4%;
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Pred. No.
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      DB 17; 1
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SOURCE
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      Query Match
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AZ405428
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Unpublished (2000)
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Location/Qualifiers
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Insert Length: 10000 Std Error:
Plate: 0174 row: D column: 13
seg_primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                             /note="Wector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil473L14) plnP129072.l), a copy-number of pWD42 (gil473L14) plnP129072.l), a copy-number and suith adaptors complementary to the insert adaptors and suite as a suite adaptors and suite adapto
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                                                                                                                         purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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/clone="UUGC1M0174D13"
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/strain="C57BL/6J"
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      0.4%;
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          DB 17; Length 26; 3.3e+04;
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